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OM nucleic - nucleic search, using sw model

Run on: April 17, 2006, 23:57:18 ; Search time 363 Seconds
(without alignments)
1475.762 Million cell updates/sec

Title: US-10-663-241-32

Perfect score: 133
Sequence: 1 gctcccccgcgcgtctcaaa.....tacagttgtagggaggatt 133

Scoring table: IDENTITY NUC
Gapop 10'0 , Gapext 1.0

Searched: 9281099 seqs, 2013915447 residues

Total number of hits satisfying chosen parameters: 18562198

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA_New:*
1: /SIDS5/ptodata/1/pubpna/US08_NEW_PUB.seq:*
2: /SIDS5/ptodata/1/pubpna/US06_NEW_PUB.seq:*
3: /SIDS5/ptodata/1/pubpna/US07_NEW_PUB.seq:*
4: /SIDS5/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
5: /SIDS5/ptodata/1/pubpna/US09_NEW_PUB.seq:*
6: /SIDS5/ptodata/1/pubpna/US10_NEW_PUB.seq:*
7: /SIDS5/ptodata/1/pubpna/US11_NEW_PUB.seq:*
8: /SIDS5/ptodata/1/pubpna/US10_NEW_PUB.seq:*
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10: /SIDS5/ptodata/1/pubpna/US10_NEW_PUB.seq:*
11: /SIDS5/ptodata/1/pubpna/US11_NEW_PUB.seq:*
12: /SIDS5/ptodata/1/pubpna/US11_NEW_PUB.seq:*
13: /SIDS5/ptodata/1/pubpna/US11_NEW_PUB.seq:*
14: /SIDS5/ptodata/1/pubpna/US11_NEW_PUB.seq:*
15: /SIDS5/ptodata/1/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	122	91.7	176	9 US-10-527-048-14	Sequence 14, Appl
2	122	91.7	5834	9 US-10-527-048-15	Sequence 15, Appl
3	122	91.7	6465	9 US-10-527-048-25	Sequence 25, Appl
4	122	91.7	6659	9 US-10-527-048-22	Sequence 22, Appl
5	122	91.7	7549	9 US-10-527-048-24	Sequence 24, Appl
6	102.8	77.3	2569	11 US-11-190-122-3	Sequence 3, Appl1
7	102.8	77.3	2800	11 US-11-190-122-1	Sequence 1, Appl1
8	102.8	77.3	3119	11 US-11-190-122-2	Sequence 2, Appl1
9	62.2	46.8	8040	11 US-11-004-399-377	Sequence 377, App
10	62.2	46.8	8082	11 US-11-004-399-378	Sequence 378, App
11	62.2	46.8	8082	11 US-11-004-399-483	Sequence 483, App
12	62.2	46.8	8082	11 US-11-004-399-605	Sequence 605, App
13	62.2	46.8	9348	11 US-11-004-399-1	Sequence 1, Appl1
14	62.2	46.8	9348	11 US-11-004-399-113	Sequence 113, App
15	62.2	46.8	9348	11 US-11-004-399-274	Sequence 274, App
16	62.2	46.8	10591	11 US-11-004-399-3593	Sequence 3593, Ap
17	62.2	46.8	10591	11 US-11-004-399-3738	Sequence 3738, Ap
18	62.2	46.8	10591	11 US-11-004-399-3916	Sequence 3916, Ap

C	19	29.4	22.1	9136	14 US-11-136-527-3808	Sequence 3808, Ap
C	20	29	21.8	7479	14 US-11-136-527-3308	Sequence 3308, Ap
C	21	27.6	20.8	507	6 US-09-925-065A-132558	Sequence 132558, Ap
C	22	27.6	20.8	507	6 US-09-925-065A-132559	Sequence 132559, Ap
C	23	27.6	20.8	507	6 US-09-925-065A-132560	Sequence 132560, Ap
C	24	27.6	20.8	518	9 US-10-301-480-284	Sequence 284, App
C	25	27.6	20.8	518	10 US-10-301-480-613693	Sequence 613693, Ap
C	26	27.6	20.8	526	10 US-10-301-480-228769	Sequence 228769, Ap
C	27	27.6	20.8	526	10 US-10-301-480-228770	Sequence 228770, Ap
C	28	27.6	20.8	526	10 US-10-301-480-228771	Sequence 228771, Ap
C	29	27.6	20.8	526	10 US-10-301-480-842178	Sequence 842178, Ap
C	30	27.6	20.8	526	10 US-10-301-480-842179	Sequence 842179, Ap
C	31	27.6	20.8	526	10 US-10-301-480-842180	Sequence 842180, Ap
C	32	27.6	20.8	1095	6 US-09-925-065A-698990	Sequence 698990, Ap
C	33	27.4	20.6	640	6 US-09-925-065A-512538	Sequence 512538, Ap
C	34	27.4	20.6	61487	14 US-11-124-3678-5103	Sequence 5103, Ap
C	35	27.2	20.5	634	9 US-10-301-480-26304	Sequence 26304, Ap
C	36	27.2	20.5	634	9 US-10-301-480-26305	Sequence 26305, Ap
C	37	27.2	20.5	634	10 US-10-301-480-639713	Sequence 639713, Ap
C	38	27.2	20.5	634	10 US-10-301-480-639714	Sequence 639714, Ap
C	39	27	20.3	533	6 US-09-925-065A-13188	Sequence 13188, A
C	40	27	20.3	533	9 US-10-301-480-114425	Sequence 114425, Ap
C	41	27	20.3	533	10 US-10-301-480-727834	Sequence 727834, Ap
C	42	27	20.3	568	6 US-09-925-065A-619601	Sequence 619601, Ap
C	43	27	20.3	985	14 US-11-136-527-1708	Sequence 1708, Ap
C	44	27	20.3	985	14 US-11-136-527-5804	Sequence 5804, Ap
C	45	27	20.3	1694969	7 US-10-506-454-1690	Sequence 1690, Ap

ALIGNMENTS

RESULT 1
US-10-527-048-14
Sequence 14, Application US/10527048
Publication No. US200600267041
GENERAL INFORMATION:
APPLICANT: Center for Genetic Engineering and Biotechnology.
TITLE OF INVENTION: VECTOR FOR PRODUCTION OF ANGIOPERM TRANSPLASTOMIC PLANTS.
FILE REFERENCE: Vector for plasmid transformation
CURRENT APPLICATION NUMBER: US/10/527,048
CURRENT FILING DATE: 2005-03-07
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 14
LENGTH: 176
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURES:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
OTHER INFORMATION: fragment codifying for the promoter region of the plasmid 16S
US-10-527-048-14
ribosomal RNA (Prrn), with added restriction sites.

Query Match 91.7%; Score 122; DB 9; Length 176;

Best Local Similarity 99.3%; Pred. No. 8.1e-11;
Matches 133; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY	1	GCTCCCCCGCGCTGTTCAATGAGATGATTAAGAGCTGTGGATTGACGTAGGGG	60
DB	16	GCTCCCCCGCGCTGTTCAATGAGATGATTAAGAGCTGTGGATTGACGTAGGGG	75
QY	61	CAGGATGAGTATA-TTCTGGAGCGAATCCGGGCGAATACGAAGCGCTGTGATACGT	119
DB	76	CAGGATGAGTATAATTCTGGAGCGAATCCGGGCGAATACGAAGCGCTGTGATACGT	135
QY	120	TGTAGGAGGAGATT	133
DB	136	TGTAGGAGGAGATT	149

RESULT 2
US-10-527-048-15

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/ Sequence 15, Application US/10527048
/ Publication No. US20060026704A1
/ GENERAL INFORMATION:
/ APPLICANT: Center for Genetic Engineering and Biotechnology.
/ TITLE OF INVENTION: VECTOR FOR PRODUCTION OF ANGIOSPERM TRANSPLASTOMIC PLANTS.
/ FILE REFERENCE: Vector for plasmid transformation
/ CURRENT APPLICATION NUMBER: US/10/527,048
/ NUMBER OF SEQ ID NOS: 26
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 1534
/ LENGTH: 5834
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Nucleotide sequence of DNA
/ OTHER INFORMATION: fragment from the vector pYTPA between the rice atpb and
/ OTHER INFORMATION: tobacco rbcL borders.
US-10-527-048-15
```

```
Query Match          91.7%; Score 122; DB 9; Length 5834;
Best Local Similarity 99.3%; Pred. No. 1.5e-30;
Matches 133; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
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```
QY 1 GCTCCCCCGCGCTGTTCAATGAGATGATAAGAGGCTGTGGATTGACGTGAGGGG 60
DB 1918 GCTCCCCCGCGCTGTTCAATGAGATGATAAGAGGCTGTGGATTGACGTGAGGGG 1977
QY 61 CAGGATGGCTATA-TTCTGGAGGCGAAGCTCCGGGGAATACGAACGCTTGATACAGT 119
DB 1978 CAGGATGGCTATAATTCTGGAGGCGAAGCTCCGGGGAATACGAACGCTTGATACAGT 2037
QY 120 TGTAGGAGGAGATT 133
DB 2038 TGTAGGAGGAGATT 2051
```

```
RESU 3
US-10-527-048-25
```

```
/ Sequence 25, Application US/10527048
/ Publication No. US20060026704A1
/ GENERAL INFORMATION:
/ APPLICANT: Center for Genetic Engineering and Biotechnology.
/ TITLE OF INVENTION: VECTOR FOR PRODUCTION OF ANGIOSPERM TRANSPLASTOMIC PLANTS.
/ FILE REFERENCE: Vector for plasmid transformation
/ CURRENT APPLICATION NUMBER: US/10/527,048
/ NUMBER OF SEQ ID NOS: 26
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 25
/ LENGTH: 6465
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Nucleotide sequence of DNA
/ OTHER INFORMATION: fragment from the vector pYTPA-Bar between the rice atpb and
/ OTHER INFORMATION: tobacco rbcL borders.
US-10-527-048-25
```

```
Query Match          91.7%; Score 122; DB 9; Length 6465;
Best Local Similarity 99.3%; Pred. No. 1.5e-30;
Matches 133; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
```

```
QY 1 GCTCCCCCGCGCTGTTCAATGAGATGATAAGAGGCTGTGGATTGACGTGAGGGG 60
DB 1918 GCTCCCCCGCGCTGTTCAATGAGATGATAAGAGGCTGTGGATTGACGTGAGGGG 1977
QY 61 CAGGATGGCTATA-TTCTGGAGGCGAAGCTCCGGGGAATACGAACGCTTGATACAGT 119
DB 1978 CAGGATGGCTATAATTCTGGAGGCGAAGCTCCGGGGAATACGAACGCTTGATACAGT 2037
QY 120 TGTAGGAGGAGATT 133
```

```
DB 2038 TGTAGGAGGAGATT 2051
```

```
RESULT 4
```

```
US-10-527-048-22
/ Sequence 22, Application US/10527048
/ Publication No. US20060026704A1
/ GENERAL INFORMATION:
/ APPLICANT: Center for Genetic Engineering and Biotechnology.
/ TITLE OF INVENTION: VECTOR FOR PRODUCTION OF ANGIOSPERM TRANSPLASTOMIC PLANTS.
/ FILE REFERENCE: Vector for plasmid transformation
/ CURRENT APPLICATION NUMBER: US/10/527,048
/ NUMBER OF SEQ ID NOS: 26
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 22
/ LENGTH: 6659
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Nucleotide sequence of DNA
/ OTHER INFORMATION: fragment from the vector pYTPA-aada between the rice atpb and
/ OTHER INFORMATION: tobacco rbcL borders.
US-10-527-048-22
```

```
Query Match          91.7%; Score 122; DB 9; Length 6659;
Best Local Similarity 99.3%; Pred. No. 1.5e-30;
Matches 133; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
```

```
QY 1 GCTCCCCCGCGCTGTTCAATGAGATGATAAGAGGCTGTGGATTGACGTGAGGGG 60
DB 1918 GCTCCCCCGCGCTGTTCAATGAGATGATAAGAGGCTGTGGATTGACGTGAGGGG 1977
QY 61 CAGGATGGCTATA-TTCTGGAGGCGAAGCTCCGGGGAATACGAACGCTTGATACAGT 119
DB 1978 CAGGATGGCTATAATTCTGGAGGCGAAGCTCCGGGGAATACGAACGCTTGATACAGT 2037
QY 120 TGTAGGAGGAGATT 133
DB 2038 TGTAGGAGGAGATT 2051
```

```
RESULT 5
```

```
US-10-527-048-24
/ Sequence 24, Application US/10527048
/ Publication No. US20060026704A1
/ GENERAL INFORMATION:
/ APPLICANT: Center for Genetic Engineering and Biotechnology.
/ TITLE OF INVENTION: VECTOR FOR PRODUCTION OF ANGIOSPERM TRANSPLASTOMIC PLANTS.
/ FILE REFERENCE: Vector for plasmid transformation
/ CURRENT APPLICATION NUMBER: US/10/527,048
/ NUMBER OF SEQ ID NOS: 26
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 24
/ LENGTH: 7549
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Nucleotide sequence of DNA
/ OTHER INFORMATION: fragment from the vector pYTPA-HB-aada between the rice atpb and
/ OTHER INFORMATION: tobacco rbcL borders.
US-10-527-048-24
```

```
Query Match          91.7%; Score 122; DB 9; Length 7549;
Best Local Similarity 99.3%; Pred. No. 1.6e-30;
Matches 133; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
```

```
QY 1 GCTCCCCCGCGCTGTTCAATGAGATGATAAGAGGCTGTGGATTGACGTGAGGGG 60
DB 2808 GCTCCCCCGCGCTGTTCAATGAGATGATAAGAGGCTGTGGATTGACGTGAGGGG 2867
QY 61 CAGGATGGCTATA-TTCTGGAGGCGAAGCTCCGGGGAATACGAACGCTTGATACAGT 119
```

```
Db      2868 CAGGATGCTATATTTCTGGAGCGAATCCGGCGCAATGCAAGCGCTTGATACAGT 2927
        |||
Qy      120 TGTAGGAGGAGATT 133
        |||
Db      2928 TGTAGGAGGAGATT 2941
```

RESULT 6

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US-11-190-122-3
; Sequence 3, Application US/11190122
; Publication No. US20060031964A1
; GENERAL INFORMATION:
; APPLICANT: Daniell, Henry
; TITLE OF INVENTION: Placid Genetic Engineering Via Somatic Embryogenesis
; FILE REFERENCE: CHL-T107C322
; CURRENT APPLICATION NUMBER: US/11/190,122
; CURRENT FILING DATE: 2005-07-25
; PRIOR APPLICATION NUMBER: 60/344,704
; PRIOR FILING DATE: 2001-12-26
; PRIOR APPLICATION NUMBER: 10/500,351
; PRIOR FILING DATE: 2004-06-25
; PRIOR APPLICATION NUMBER: pct/us2003/021157
; PRIOR FILING DATE: 2003-07-03
; PRIOR APPLICATION NUMBER: 60/590,848
; PRIOR FILING DATE: 2004-07-23
; PRIOR APPLICATION NUMBER: 60/590,751
; PRIOR FILING DATE: 2004-07-23
; PRIOR APPLICATION NUMBER: 10/519,821
; PRIOR FILING DATE: 2004-12-30
; PRIOR APPLICATION NUMBER: 60/400,816
; PRIOR FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: 60/393,651
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: 60/393,428
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: PCT/US2002/041503
; PRIOR FILING DATE: 2002-12-26
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 2569
; TYPE: DNA
; ORGANISM: ARTIFICIAL
; FEATURE:
; OTHER INFORMATION: apha-6/nptII expression cassette
US-11-190-122-3
```

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Query Match      77.3%; Score 102.8; DB 11; Length 2569;
Best Local Similarity 90.3%; Pred. No. 3,1e-24;
Matches 121; Conservative 0; Mismatches 12; Indels 1; Gaps 1;
```

```
Qy      1 GCTCCCCCGCGCTGTTCAATGAGATGATTAAGAGCGCTGTGGGATTGACGTGAGGGGG 60
        |||
Db      79 GCTCCCCCGCGCTGTTCAATGAGATGATTAAGAGCGCTGTGGGATTGACGTGAGGGGG 138
        |||
Qy      61 CAGGATGCTATATTTCTGGAGCGAATCCGGCGCAATGCAAGCGCTTGATACAGT 119
        |||
Db      139 CAGGATGCTATATTTCTGGAGCGAATCCGGCGCAATGCAAGCGCTTGATACAG 198
        |||
Qy      120 TGTAGGAGGAGATT 133
        |||
Db      199 TGTAGGAGGAGATT 212
```

RESULT 7

```
US-11-190-122-1
; Sequence 1, Application US/11190122
; Publication No. US20060031964A1
; GENERAL INFORMATION:
; APPLICANT: Daniell, Henry
; TITLE OF INVENTION: Placid Genetic Engineering Via Somatic Embryogenesis
; FILE REFERENCE: CHL-T107C322
```

```
; CURRENT APPLICATION NUMBER: US/11/190,122
; CURRENT FILING DATE: 2005-07-25
; PRIOR APPLICATION NUMBER: 60/344,704
; PRIOR FILING DATE: 2001-12-26
; PRIOR APPLICATION NUMBER: 10/500,351
; PRIOR FILING DATE: 2004-06-25
; PRIOR APPLICATION NUMBER: pct/us2003/021157
; PRIOR FILING DATE: 2003-07-03
; PRIOR APPLICATION NUMBER: 60/590,848
; PRIOR FILING DATE: 2004-07-23
; PRIOR APPLICATION NUMBER: 60/590,751
; PRIOR FILING DATE: 2004-07-23
; PRIOR APPLICATION NUMBER: 10/519,821
; PRIOR FILING DATE: 2004-12-30
; PRIOR APPLICATION NUMBER: 60/400,816
; PRIOR FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: 60/393,651
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: 60/393,428
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: PCT/US2002/041503
; PRIOR FILING DATE: 2002-12-26
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 2800
; TYPE: DNA
; ORGANISM: ARTIFICIAL
; FEATURE:
; OTHER INFORMATION: aada/BADH expression cassette
US-11-190-122-1
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Query Match      77.3%; Score 102.8; DB 11; Length 2800;
Best Local Similarity 90.3%; Pred. No. 3,2e-24;
Matches 121; Conservative 0; Mismatches 12; Indels 1; Gaps 1;
```

```
Qy      1 GCTCCCCCGCGCTGTTCAATGAGATGATTAAGAGCGCTGTGGGATTGACGTGAGGGGG 60
        |||
Db      85 GCTCCCCCGCGCTGTTCAATGAGATGATTAAGAGCGCTGTGGGATTGACGTGAGGGGG 144
        |||
Qy      61 CAGGATGCTATATTTCTGGAGCGAATCCGGCGCAATGCAAGCGCTTGATACAGT 119
        |||
Db      145 CAGGATGCTATATTTCTGGAGCGAATCCGGCGCAATGCAAGCGCTTGATACAG 204
        |||
Qy      120 TGTAGGAGGAGATT 133
        |||
Db      205 TGTAGGAGGAGATT 218
```

RESULT 8

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US-11-190-122-2
; Sequence 2, Application US/11190122
; Publication No. US20060031964A1
; GENERAL INFORMATION:
; APPLICANT: Daniell, Henry
; TITLE OF INVENTION: Placid Genetic Engineering Via Somatic Embryogenesis
; FILE REFERENCE: CHL-T107C322
; CURRENT APPLICATION NUMBER: US/11/190,122
; CURRENT FILING DATE: 2005-07-25
; PRIOR APPLICATION NUMBER: 60/344,704
; PRIOR FILING DATE: 2001-12-26
; PRIOR APPLICATION NUMBER: 10/500,351
; PRIOR FILING DATE: 2004-06-25
; PRIOR APPLICATION NUMBER: pct/us2003/021157
; PRIOR FILING DATE: 2003-07-03
; PRIOR APPLICATION NUMBER: 60/590,848
; PRIOR FILING DATE: 2004-07-23
; PRIOR APPLICATION NUMBER: 60/590,751
; PRIOR FILING DATE: 2004-07-23
; PRIOR APPLICATION NUMBER: 10/519,821
; PRIOR FILING DATE: 2004-12-30
; PRIOR APPLICATION NUMBER: 60/400,816
; PRIOR FILING DATE: 2002-08-02
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PRIOR APPLICATION NUMBER: 60/393,651
PRIOR FILING DATE: 2002-07-03
PRIOR APPLICATION NUMBER: 60/393,428
PRIOR FILING DATE: 2002-07-03
PRIOR APPLICATION NUMBER: PCT/US2002/041503
PRIOR FILING DATE: 2002-12-26
NUMBER OF SEQ ID NOS: 21
SOFTWARE: PatentIn version 3.2
SEQ ID NO 2
LENGTH: 3119
TYPE: DNA
ORGANISM: ARTIFICIAL
FEATURE:
OTHER INFORMATION: gfp/BADH expression cassette
US-11-190-122-2

Query Match 77.3%; Score 102.8; DB 11; Length 3119;
Best Local Similarity 90.3%; Pred. No. 3.2e-24;
Matches 121; Conservative 0; Mismatches 12; Indels 1; Gaps 1;

QY 1 GCTCCCCCGCTTCATAGATGAGTGAAGGCTCGTGGATTGACGTGAGGGGG 60
DB 79 GCTCCCCCGCTTCATAGATGAGTGAAGGCTCGTGGATTGACGTGAGGGGG 138
QY 61 CAGGATGGCTATA-TTCTGGAGCGAACTCCGGCGAATACGACGCTTGATACAGT 119
DB 139 CAGGATGGCTATA-TTCTGGAGCGAACTCCGGCGAATACGACGCTTGATACAG 198
QY 120 TGTAGGAGGAGT 133
DB 199 TTATGCTTGAAT 212

RESULT 9

US-11-004-399-377
Sequence 377, Application US/11004399
Publication No. US20060053516A1
GENERAL INFORMATION:
APPLICANT: Chye, Mee Lee
APPLICANT: Li, Hong Ye
APPLICANT: Ramalingam, Sathiskumar
APPLICANT: Poon, Leo Lit Man
TITLE OF INVENTION: Genetically Modified Plants Comprising SARS-CoV Viral Nucleotide
TITLE OF INVENTION: Sequences and Methods of Use Thereof For Immunization Against SA
FILE REFERENCE: 2587/73166/RDX
CURRENT APPLICATION NUMBER: US/11/004,399
PRIOR FILING DATE: 2004-12-03
PRIOR APPLICATION NUMBER: US 60/527,637
PRIOR FILING DATE: 2003-12-03
NUMBER OF SEQ ID NOS: 4043
SOFTWARE: PatentIn version 3.1
SEQ ID NO 377
LENGTH: 8040
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: pCV8
US-11-004-399-377

Query Match 46.8%; Score 62.2; DB 11; Length 8040;
Best Local Similarity 73.2%; Pred. No. 1.2e-10;
Matches 93; Conservative 0; Mismatches 33; Indels 1; Gaps 1;

QY 4 CCCCCCGCTTCATAGATGAGTGAAGGCTCGTGGATTGACGTGAGGGGGCG 63
DB 3284 CCCCCCGCTTCATAGATGAGTGAAGGCTCGTGGATTGACGTGAGGGGGCG 3343
QY 64 GGATGGCTATA-TTCTGGAGCGAACTCCGGCGAATACGACGCTTGATACAGTGT 122
DB 3344 GGATGGCTATA-TTCTGGAGCGAACTCCGGCGAATACGACGCTTGATACAGTGT 3403
QY 123 AGGAGG 129

DB 3404 AGGAGG 3410

RESULT 10

US-11-004-399-378
Sequence 378, Application US/11004399
Publication No. US20060053516A1
GENERAL INFORMATION:
APPLICANT: Chye, Mee Lee
APPLICANT: Li, Hong Ye
APPLICANT: Ramalingam, Sathiskumar
APPLICANT: Poon, Leo Lit Man
TITLE OF INVENTION: Genetically Modified Plants Comprising SARS-CoV Viral Nucleotide
TITLE OF INVENTION: Sequences and Methods of Use Thereof For Immunization Against S
FILE REFERENCE: 2587/73166/RDX
CURRENT APPLICATION NUMBER: US/11/004,399
PRIOR FILING DATE: 2004-12-03
PRIOR APPLICATION NUMBER: US 60/527,637
PRIOR FILING DATE: 2003-12-03
NUMBER OF SEQ ID NOS: 4043
SOFTWARE: PatentIn version 3.1
SEQ ID NO 378
LENGTH: 8082
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: pCV8
NAME/KEY: CDS
LOCATION: (1)..(8082)
OTHER INFORMATION:
US-11-004-399-378

Query Match 46.8%; Score 62.2; DB 11; Length 8082;
Best Local Similarity 73.2%; Pred. No. 1.2e-10;
Matches 93; Conservative 0; Mismatches 33; Indels 1; Gaps 1;

QY 4 CCCCCCGCTTCATAGATGAGTGAAGGCTCGTGGATTGACGTGAGGGGGCG 63
DB 3326 CCCCCCGCTTCATAGATGAGTGAAGGCTCGTGGATTGACGTGAGGGGGCG 3385
QY 64 GGATGGCTATA-TTCTGGAGCGAACTCCGGCGAATACGACGCTTGATACAGTGT 122
DB 3386 GGATGGCTATA-TTCTGGAGCGAACTCCGGCGAATACGACGCTTGATACAGTGT 3445
QY 123 AGGAGG 129
DB 3446 AGGAGG 3452

RESULT 11

US-11-004-399-483
Sequence 483, Application US/11004399
Publication No. US20060053516A1
GENERAL INFORMATION:
APPLICANT: Chye, Mee Lee
APPLICANT: Li, Hong Ye
APPLICANT: Ramalingam, Sathiskumar
APPLICANT: Poon, Leo Lit Man
TITLE OF INVENTION: Genetically Modified Plants Comprising SARS-CoV Viral Nucleotide
TITLE OF INVENTION: Sequences and Methods of Use Thereof For Immunization Against S
FILE REFERENCE: 2587/73166/RDX
CURRENT APPLICATION NUMBER: US/11/004,399
PRIOR FILING DATE: 2004-12-03
PRIOR APPLICATION NUMBER: US 60/527,637
PRIOR FILING DATE: 2003-12-03
NUMBER OF SEQ ID NOS: 4043
SOFTWARE: PatentIn version 3.1
SEQ ID NO 483
LENGTH: 8082

TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: pcv8
NAME/KEY: CDS
LOCATION: (2)..(8080)
OTHER INFORMATION:
US-11-004-399-483

Query Match 46.8%; Score 62.2; DB 11; Length 8082;
Best Local Similarity 73.2%; Pred. No. 1.2e-10;
Matches 93; Conservative 0; Mismatches 33; Indels 1; Gaps 1;

QY 4 CCCCCCGCTGTTCAATGAGATGATGATGAGGCTCGTGGGATTGACGTGAGGGGGCAG 63
DB 3326 CCCCCCGCATGCAAGCGAATGATGATGAGGCTTGTGGGATTGACGTGATGAGGTTAG 3385
QY 64 GGATGGCTATA-TTCTGGAGCGAATCCGGCGGAATACGAAGCGCTTGATACAGTTGT 122
DB 3386 GGTTGGCTATACGTGCTGGTGGCGAATCCAGGCTAATATCTGAAGCGCTTGAAAGTTGT 3445
QY 123 AGGAGG 129
DB 3446 AGGAGG 3452

RESULT 12

US-11-004-399-605
Sequence 605, Application US/11004399
Publication No. US20060053516A1
GENERAL INFORMATION:
APPLICANT: Chye, Mee Lee
APPLICANT: Li, Hong Ye
APPLICANT: Ramalingam, Sathiskumar
APPLICANT: Poon, Leo Lit Man
APPLICANT: Peiris, Joseph Sriyal Malik
TITLE OF INVENTION: Genetically Modified Plants Comprising SARS-CoV Viral Nucleotide
FILE REFERENCE: 2587/73166/RDX
CURRENT APPLICATION NUMBER: US/11/004,399
CURRENT FILING DATE: 2004-12-03
PRIOR APPLICATION NUMBER: US 60/527,637
PRIOR FILING DATE: 2003-12-03
NUMBER OF SEQ ID NOS: 4043
SOFTWARE: PatentIn version 3.1
SEQ ID NO 605
LENGTH: 8082
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: pcv8
NAME/KEY: CDS
LOCATION: (3)..(8081)
OTHER INFORMATION:
US-11-004-399-605

Query Match 46.8%; Score 62.2; DB 11; Length 8082;
Best Local Similarity 73.2%; Pred. No. 1.2e-10;
Matches 93; Conservative 0; Mismatches 33; Indels 1; Gaps 1;

QY 4 CCCCCCGCTGTTCAATGAGATGATGATGAGGCTCGTGGGATTGACGTGAGGGGGCAG 63
DB 3326 CCCCCCGCATGCAAGCGAATGATGATGAGGCTTGTGGGATTGACGTGATGAGGTTAG 3385
QY 64 GGATGGCTATA-TTCTGGAGCGAATCCGGCGGAATACGAAGCGCTTGATACAGTTGT 122
DB 3386 GGTTGGCTATACGTGCTGGTGGCGAATCCAGGCTAATATCTGAAGCGCTTGAAAGTTGT 3445
QY 123 AGGAGG 129
DB 3446 AGGAGG 3452

RESULT 13
US-11-004-399-1
Sequence 1, Application US/11004399
Publication No. US20060053516A1
GENERAL INFORMATION:
APPLICANT: Chye, Mee Lee
APPLICANT: Li, Hong Ye
APPLICANT: Ramalingam, Sathiskumar
APPLICANT: Poon, Leo Lit Man
APPLICANT: Peiris, Joseph Sriyal Malik
TITLE OF INVENTION: Genetically Modified Plants Comprising SARS-CoV Viral Nucleotide
FILE REFERENCE: 2587/73166/RDX
CURRENT APPLICATION NUMBER: US/11/004,399
CURRENT FILING DATE: 2004-12-03
PRIOR APPLICATION NUMBER: US 60/527,637
PRIOR FILING DATE: 2003-12-03
NUMBER OF SEQ ID NOS: 4043
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 9348
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: pcv1
NAME/KEY: CDS
LOCATION: (1)..(9348)
OTHER INFORMATION:
US-11-004-399-1

Query Match 46.8%; Score 62.2; DB 11; Length 9348;
Best Local Similarity 73.2%; Pred. No. 1.2e-10;
Matches 93; Conservative 0; Mismatches 33; Indels 1; Gaps 1;

QY 4 CCCCCCGCTGTTCAATGAGATGATGATGAGGCTCGTGGGATTGACGTGAGGGGGCAG 63
DB 4592 CCCCCCGCATGCAAGCGAATGATGATGAGGCTTGTGGGATTGACGTGATGAGGTTAG 4651
QY 64 GGATGGCTATA-TTCTGGAGCGAATCCGGCGGAATACGAAGCGCTTGATACAGTTGT 122
DB 4652 GGTTGGCTATACGTGCTGGTGGCGAATCCAGGCTAATATCTGAAGCGCTTGAAAGTTGT 4711
QY 123 AGGAGG 129
DB 4712 AGGAGG 4718

RESULT 14

US-11-004-399-113
Sequence 113, Application US/11004399
Publication No. US20060053516A1
GENERAL INFORMATION:
APPLICANT: Chye, Mee Lee
APPLICANT: Li, Hong Ye
APPLICANT: Ramalingam, Sathiskumar
APPLICANT: Poon, Leo Lit Man
APPLICANT: Peiris, Joseph Sriyal Malik
TITLE OF INVENTION: Genetically Modified Plants Comprising SARS-CoV Viral Nucleotide
FILE REFERENCE: 2587/73166/RDX
CURRENT APPLICATION NUMBER: US/11/004,399
CURRENT FILING DATE: 2004-12-03
PRIOR APPLICATION NUMBER: US 60/527,637
PRIOR FILING DATE: 2003-12-03
NUMBER OF SEQ ID NOS: 4043
SOFTWARE: PatentIn version 3.1
SEQ ID NO 113
LENGTH: 9348
TYPE: DNA
ORGANISM: Artificial Sequence

FEATURE:
OTHER INFORMATION: pcv1
FEATURE:
NAME/KEY: CDS
LOCATION: (2)..(9346)
OTHER INFORMATION:
US-11-004-399-113

Query Match 46.8%; Score 62.2; DB 11; Length 9348;
Best Local Similarity 73.2%; Pred. No. 1.2e-10;
Matches 93; Conservative 0; Mismatches 33; Indels 1; Gaps 1;

QY 4 CCCCCCGCTGTTCAATGAGATGAGAGCTGTGGATTGACGTGAGGGGACAG 63
DB 4592 CCCCCCGCAAGATCGAAGCGGATGATAGAGCTTGTGGATTGACGTGATAGGGTAG 4651
QY 64 GGATGCTATA-TTCTGGAGCGCACTCCGGGCGAATACGAGCGCTTGATACAGTTGT 122
DB 4652 GGTGGCTATACGTGCTGGCGCACTCCAGCTTAATCTGAGCGCTTGAGAGTTGT 4711
QY 123 AGGAGG 129
DB 4712 AGGAGG 4718

RESULT 15

US-11-004-399-274
Sequence 274, Application US/11004399
Publication No. US2006053516A1
GENERAL INFORMATION:
APPLICANT: Chye, Mee Lee
APPLICANT: Li, Hong Ye
APPLICANT: Ramalingam, Sachikumar
APPLICANT: Poon, Leo Lit Man
APPLICANT: Beiris, Joseph Sriyal Malik
TITLE OF INVENTION: Genetically Modified Plants Comprising SARS-CoV Viral Nucleotide
FILE REFERENCE: 2587/73166/RDK
CURRENT APPLICATION NUMBER: US/11/004,399
CURRENT FILING DATE: 2004-12-03
PRIOR APPLICATION NUMBER: US 60/527,637
PRIOR FILING DATE: 2003-12-03
NUMBER OF SEQ ID NOS: 4043
SOFTWARE: PatentIn version 3.1
SEQ ID NO 274
LENGTH: 9348
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: pcv1
FEATURE:
NAME/KEY: CDS
LOCATION: (3)..(9347)
OTHER INFORMATION:
US-11-004-399-274

Query Match 46.8%; Score 62.2; DB 11; Length 9348;
Best Local Similarity 73.2%; Pred. No. 1.2e-10;
Matches 93; Conservative 0; Mismatches 33; Indels 1; Gaps 1;

QY 4 CCCCCCGCTGTTCAATGAGATGAGAGCTGTGGATTGACGTGAGGGGACAG 63
DB 4592 CCCCCCGCAAGATCGAAGCGGATGATAGAGCTTGTGGATTGACGTGATAGGGTAG 4651
QY 64 GGATGCTATA-TTCTGGAGCGCACTCCGGGCGAATACGAGCGCTTGATACAGTTGT 122
DB 4652 GGTGGCTATACGTGCTGGCGCACTCCAGCTTAATCTGAGCGCTTGAGAGTTGT 4711
QY 123 AGGAGG 129
DB 4712 AGGAGG 4718

Search completed: April 18, 2006, 00:03:30
Job time : 365 secs

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OM nucleic - nucleic search, using sw model

Run on: April 17, 2006, 23:49:25 ; Search time 454 Seconds
(without alignments)
2422.527 Million cell updates/sec

Title: US-10-663-241-32

Perfect score: 133
Sequence: 1 gctcccccgcgcgtctcaaa.....tacagttcgtaggaaggatt 133

Scoring table: IDENTITY NUC
Gapex 10'-0', Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA.Main:*
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10: /cgn2_6/ptodaca/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	133	100.0	133	7	US-10-663-241-32
2	122	91.7	1143	6	US-10-460-716-2
3	122	91.7	1417	6	US-10-460-716-3
4	121	91.0	2145	7	US-10-473-207-26
5	119.4	89.8	1544	7	US-10-473-207-4
6	119.4	89.8	2391	7	US-10-473-207-25
7	107	80.5	119	8	US-10-881-813-6
8	102.8	77.3	220	7	US-10-095-514-3
9	102.8	77.3	233	8	US-10-737-251-38
10	102.8	77.3	6477	7	US-10-377-134-63
11	102.8	77.3	7652	7	US-10-680-824A-19
12	102.8	77.3	8684	7	US-10-680-824A-1
13	102.8	77.3	10011	7	US-10-680-824A-19
14	102.8	77.3	10011	9	US-10-957-562-4
15	96.2	72.3	8684	7	US-10-680-824A-2
16	94	70.7	183	6	US-10-258-253-16
17	93.2	70.1	223	6	US-10-737-251-41
18	91.6	68.9	234	8	US-10-737-251-41
19	87.4	65.7	202	3	US-09-843-324A-2
20	87.4	65.7	244	3	US-09-843-324A-1
21	83.6	63.0	112	8	US-10-737-251-3
22	83.6	62.9	237	8	US-10-737-251-43
23	83.6	62.9	1993	6	US-10-460-716-1

C	24	83.6	62.9	4586	6	US-10-460-716-4	Sequence 4, Appl
C	25	83.6	62.9	7455	5	US-10-219-227-19	Sequence 19, Appl
C	26	82.2	61.8	112	8	US-10-737-251-22	Sequence 22, Appl
C	27	80.8	60.8	112	8	US-10-737-251-4	Sequence 4, Appl
C	28	80.6	60.6	112	8	US-10-737-251-21	Sequence 21, Appl
C	29	80.6	60.6	112	8	US-10-737-251-23	Sequence 23, Appl
C	30	79	59.4	112	8	US-10-737-251-5	Sequence 5, Appl
C	31	79	59.4	112	8	US-10-737-251-6	Sequence 6, Appl
C	32	79	59.4	112	8	US-10-737-251-7	Sequence 7, Appl
C	33	79	59.4	112	8	US-10-737-251-8	Sequence 8, Appl
C	34	79	59.4	112	8	US-10-737-251-9	Sequence 9, Appl
C	35	79	59.4	112	8	US-10-737-251-10	Sequence 10, Appl
C	36	79	59.4	112	8	US-10-737-251-11	Sequence 11, Appl
C	37	79	59.4	112	8	US-10-737-251-12	Sequence 12, Appl
C	38	79	59.4	112	8	US-10-737-251-13	Sequence 13, Appl
C	39	79	59.4	112	8	US-10-737-251-14	Sequence 14, Appl
C	40	79	59.4	112	8	US-10-737-251-15	Sequence 15, Appl
C	41	79	59.4	112	8	US-10-737-251-16	Sequence 16, Appl
C	42	79	59.4	112	8	US-10-737-251-17	Sequence 17, Appl
C	43	79	59.4	112	8	US-10-737-251-18	Sequence 18, Appl
C	44	79	59.4	112	8	US-10-737-251-19	Sequence 19, Appl
C	45	79	59.4	112	8	US-10-737-251-20	Sequence 20, Appl

ALIGNMENTS

RESULT 1
US-10-663-241-32
; Sequence 32, Application US/10663241
; Publication No. US20040040058A1
; GENERAL INFORMATION:
; APPLICANT: Malliga, Pal
; APPLICANT: Srilaxmi, Daniel
; TITLE OR INVENTION: Placids Promoters for Transgene
; FILE REFERENCE: RUC 97-0097
; CURRENT APPLICATION NUMBER: US/10/663,241
; CURRENT FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: US/09/445,283C
; PRIOR FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: PCT/US98/11437
; PRIOR FILING DATE: 1998-06-03
; PRIOR APPLICATION NUMBER: 60/058,670
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/048,376
; PRIOR FILING DATE: 1997-06-03
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 32
; LENGTH: 133
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Prrn promoter
US-10-663-241-32

Query Match 100.0%; Score 133; DB 7; Length 133;
Best Local Similarity 100.0%; Pred. No. 1.3e-39;
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	GCTCCCCCGCGCTTCATGAGTGGTATAGAGGCTCGTGGATTGACGAGGGGG	60
DB	1	GCTCCCCCGCGCTTCATGAGTGGTATAGAGGCTCGTGGATTGACGAGGGGG	60
QY	61	CAGGATGCTATATTCTGGAGCGAATCTCCGGCGAATACGAAGCGCTTGATACATT	120
DB	61	CAGGATGCTATATTCTGGAGCGAATCTCCGGCGAATACGAAGCGCTTGATACATT	120
QY	121	GTAGGAGGAGATT	133
DB	121	GTAGGAGGAGATT	133

```
RESULT 2
US-10-460-716-2/c
; Sequence 2, Application US/10460716
; Publication No. US20030200568A1
; GENERAL INFORMATION:
; APPLICANT: Maliga, Pal
; APPLICANT: Skarjinskaja, Marina
; APPLICANT: Svab, Zora
; APPLICANT: Rutgers, The State University of New Jersey
; TITLE OF INVENTION: Plasmid Transformation in Legnerella
; FILE REFERENCE: Rut 00-0109CIP
; CURRENT APPLICATION NUMBER: US/10/460, 716
; PRIOR FILING DATE: 2003-06-12
; PRIOR APPLICATION NUMBER: US/09/524, 087A
; PRIOR FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: PCT/US97/03444
; PRIOR FILING DATE: 1997-03-06
; PRIOR APPLICATION NUMBER: 60/102, 716
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 1143
; TYPE: DNA
; ORGANISM: Nicotinium tobacum
US-10-460-716-2

Query Match          91.7%; Score 122; DB 6; Length 1143;
Best Local Similarity 99.3%; Pred. No. 2, 8e-35;
Matches 133; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY      1  GCTCCCCCGCCGCTGCTCAATGAGATGATTAAGAGGCTCGTGGATTGACCTGAGGGG 60
DB      1130 GCTCCCCCGCCGCTGCTCAATGAGATGATTAAGAGGCTCGTGGATTGACCTGAGGGG 1071

QY      61  CAGGATGGCTATA-TTCTGGAGCGAACTCCGGCGGAATACGAGCGCTTGATCACT 119
DB      1070 CAGGATGGCTATATTCTCGGAGCGAACTCCGGCGGAATACGAGCGCTTGATCACT 1011

QY      120 TGTAGGAGGAGATT 133
DB      1010 TGTAGGAGGAGATT 997

RESULT 3
US-10-460-716-3
; Sequence 3, Application US/10460716
; Publication No. US20030200568A1
; GENERAL INFORMATION:
; APPLICANT: Maliga, Pal
; APPLICANT: Skarjinskaja, Marina
; APPLICANT: Svab, Zora
; APPLICANT: Rutgers, The State University of New Jersey
; TITLE OF INVENTION: Plasmid Transformation in Legnerella
; FILE REFERENCE: Rut 00-0109CIP
; CURRENT APPLICATION NUMBER: US/10/460, 716
; PRIOR FILING DATE: 2003-06-12
; PRIOR APPLICATION NUMBER: US/09/524, 087A
; PRIOR FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: PCT/US97/03444
; PRIOR FILING DATE: 1997-03-06
; PRIOR APPLICATION NUMBER: 60/102, 716
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 1417
; TYPE: DNA
; ORGANISM: Artificial Sequence
```

```
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-10-460-716-3

Query Match          91.7%; Score 122; DB 6; Length 1417;
Best Local Similarity 99.3%; Pred. No. 3e-35;
Matches 133; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY      1  GCTCCCCCGCCGCTGCTCAATGAGATGATTAAGAGGCTCGTGGATTGACCTGAGGGG 60
DB      23  GCTCCCCCGCCGCTGCTCAATGAGATGATTAAGAGGCTCGTGGATTGACCTGAGGGG 82

QY      61  CAGGATGGCTATA-TTCTGGAGCGAACTCCGGCGGAATACGAAAGCGCTTGATCACT 119
DB      83  CAGGATGGCTATATTCTCGGAGCGAACTCCGGCGGAATACGAAAGCGCTTGATCACT 142

QY      120 TGTAGGAGGAGATT 133
DB      143 TGTAGGAGGAGATT 156

RESULT 4
US-10-473-207-26
; Sequence 26, Application US/10473207
; Publication No. US20040163145A1
; GENERAL INFORMATION:
; APPLICANT: Maliga, Pal
; APPLICANT: Cornille, Sylvie
; APPLICANT: Lutz, Kerry
; TITLE OF INVENTION: Integrases for the insertion of
; FILE REFERENCE: 1594-RUT.01-091US
; CURRENT APPLICATION NUMBER: US/10/473, 207
; PRIOR FILING DATE: 2003-09-19
; PRIOR APPLICATION NUMBER: PCT/US02/09537
; PRIOR FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: 60/279615
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 26
; LENGTH: 2145
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: plasmid fragment
US-10-473-207-26

Query Match          91.0%; Score 121; DB 7; Length 2145;
Best Local Similarity 99.2%; Pred. No. 7, 7e-35;
Matches 132; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY      1  GCTCCCCCGCCGCTGCTCAATGAGATGATTAAGAGGCTCGTGGATTGACCTGAGGGG 60
DB      17  GCTCCCCCGCCGCTGCTCAATGAGATGATTAAGAGGCTCGTGGATTGACCTGAGGGG 76

QY      61  CAGGATGGCTATA-TTCTGGAGCGAACTCCGGCGGAATACGAAAGCGCTTGATCACT 119
DB      77  CAGGATGGCTATATTCTCGGAGCGAACTCCGGCGGAATACGAAAGCGCTTGATCACT 136

QY      120 TGTAGGAGGAGATT 132
DB      137 TGTAGGAGGAGATT 149

RESULT 5
US-10-473-207-4/c
; Sequence 4, Application US/10473207
; Publication No. US20040163145A1
; GENERAL INFORMATION:
; APPLICANT: Maliga, Pal
; APPLICANT: Cornille, Sylvie
; APPLICANT: Lutz, Kerry
```


;; TITLE OF INVENTION: Integrases for the insertion of
;; FILE REFERENCE: heterologous nucleic acids into the plasmid genome
;; CURRENT FILING DATE: 2003-09-19
;; PRIOR APPLICATION NUMBER: PCT/US02/09537
;; PRIOR FILING DATE: 2002-03-29
;; PRIOR APPLICATION NUMBER: 60/279615
;; NUMBER OF SEQ ID NOS: 29
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 4
;; LENGTH: 1544
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: vector insert
US-10-473-207-4

Query Match 89.8%; Score 119.4; DB 7; Length 1544;
Best Local Similarity 98.5%; Pred. No. 2.9e-34;
Matches 131; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 GCTCCCCCGCGCTGTTCAATGAGATGATAGAGGCTGCTGGATTGACGTGAGGGG 60
DB 1393 GCTCCCCCGCGCTGTTCAATGAGATGATAGAGGCTGCTGGATTGACGTGAGGGG 1334
QY 61 CAGGATGGCTATA-TTCTGGAGCGAATCCGGGGCAATACGAGGCTTGGATACGT 119
DB 1333 CAGGATGGCTATA-TTCTGGAGCGAATCCGGGGCAATACGAGGCTTGGATACGT 1274
QY 120 TGTAGGAGGGAT 132
DB 1273 TGTAGGAGGGAT 1261

RESULT 6

US-10-473-207-25
;; Sequence 25, Application US/10473207
;; Publication No. US20040163145A1
;; GENERAL INFORMATION:
;; APPLICANT: Maliga, Pal
;; APPLICANT: Cornille, Sylvie
;; APPLICANT: Lutz, Kerry
;; TITLE OF INVENTION: Integrases for the insertion of
;; FILE REFERENCE: 1594-RUT-01-091US
;; CURRENT FILING DATE: 2003-09-19
;; PRIOR APPLICATION NUMBER: PCT/US02/09537
;; PRIOR FILING DATE: 2002-03-29
;; PRIOR APPLICATION NUMBER: 60/279615
;; NUMBER OF SEQ ID NOS: 29
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 25
;; LENGTH: 2391
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: plasmid fragment
US-10-473-207-25

Query Match 89.8%; Score 119.4; DB 7; Length 2391;
Best Local Similarity 98.5%; Pred. No. 3.1e-34;
Matches 131; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 GCTCCCCCGCGCTGTTCAATGAGATGATAGAGGCTGCTGGATTGACGTGAGGGG 60
DB 13 GCTCCCCCGCGCTGTTCAATGAGATGATAGAGGCTGCTGGATTGACGTGAGGGG 72
QY 61 CAGGATGGCTATA-TTCTGGAGCGAATCCGGGGCAATACGAGGCTTGGATACGT 119

DB 73 CAGGATGGCTATA-TTCTGGAGCGAATCCGGGGCAATACGAGGCTTGGATACGT 132
QY 120 TGTAGGAGGGAT 132
DB 133 TGTAGGAGGGAT 145

RESULT 7

US-10-881-813-6
;; Sequence 6, Application US/10881813
;; Publication No. US20050044593A1
;; GENERAL INFORMATION:
;; APPLICANT: Cox, Kevin
;; APPLICANT: Peeler, Charles G.
;; TITLE OF INVENTION: Chloroplast Transformation of Duckweed
;; FILE REFERENCE: 40989/279944
;; CURRENT APPLICATION NUMBER: US/10/881,813
;; CURRENT FILING DATE: 2004-06-30
;; PRIOR APPLICATION NUMBER: US 60/484,166
;; PRIOR FILING DATE: 2003-07-01
;; PRIOR APPLICATION NUMBER: US 60/492,179
;; NUMBER OF SEQ ID NOS: 12
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 6
;; LENGTH: 119
;; TYPE: DNA
;; ORGANISM: Nicotiana tabacum
US-10-881-813-6

Query Match 80.5%; Score 107; DB 8; Length 119;
Best Local Similarity 99.2%; Pred. No. 7.7e-30;
Matches 118; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 GCTCCCCCGCGCTGTTCAATGAGATGATAGAGGCTGCTGGATTGACGTGAGGGG 60
DB 1 GCTCCCCCGCGCTGTTCAATGAGATGATAGAGGCTGCTGGATTGACGTGAGGGG 60
QY 61 CAGGATGGCTATA-TTCTGGAGCGAATCCGGGGCAATACGAGGCTTGGATACGT 118
DB 61 CAGGATGGCTATA-TTCTGGAGCGAATCCGGGGCAATACGAGGCTTGGATACGT 119

RESULT 8

US-10-095-514-3
;; Sequence 3, Application US/10095514
;; Publication No. US20040093658A1
;; GENERAL INFORMATION:
;; APPLICANT: Sasaki, Yukiko
;; APPLICANT: Yokota, Akiko
;; APPLICANT: Madoka, Yuka
;; TITLE OF INVENTION: Method for Promoting Fatty Acid Synthesis in a Plant
;; FILE REFERENCE: 026350-072
;; CURRENT APPLICATION NUMBER: US/10/095,514
;; CURRENT FILING DATE: 2002-03-13
;; PRIOR APPLICATION NUMBER: JP 2001-70,691
;; PRIOR FILING DATE: 2001-03-13
;; PRIOR APPLICATION NUMBER: JP 2001-300,038
;; NUMBER OF SEQ ID NOS: 11
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 3
;; LENGTH: 220
;; TYPE: DNA
;; ORGANISM: N. tabacum cv. Xanthi
US-10-095-514-3

Query Match 77.3%; Score 102.8; DB 7; Length 220;
Best Local Similarity 90.3%; Pred. No. 3.3e-28;
Matches 121; Conservative 0; Mismatches 12; Indels 1; Gaps 1;

QY 1 GCTCCCCCGCGCTGTTCAATGAGATGATAGAGGCTGCTGGATTGACGTGAGGGG 60

```

PRIOR FILING DATE: 1999-05-24
NUMBER OF SEQ ID NOS: 138
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 63
LENGTH: 6477
TYPE: DNA
ORGANISM: Unknown
FEATURES:
OTHER INFORMATION: Nucleotides 1-2482: E. coli vector pUTMUS28 (New
OTHER INFORMATION: England Biolabs, Inc.)
FEATURES:
OTHER INFORMATION: Nucleotides 2493-6242: Nicotiana tabacum
FEATURES:
OTHER INFORMATION: Nucleotides 6243-6477: E. coli vector pUTMUS28
OTHER INFORMATION: (New England Biolabs, Inc.)
US-10-377-134-63

Query Match 77.3%; Score 102.8; DB 7; Length 6477;
Best Local Similarity 90.3%; Pred. No. 6,7e-28;
Matches 121; Conservative 0; Mismatches 12; Indels 1; Gaps 1;

Cy 1 GCTCCCCCGCGCTTCATAGATGAGTGAAGAGGCTGTGGGATTGACGTGAGGGG 60
Db GCTCCCCCGCGCTTCATAGATGAGTGAAGAGGCTGTGGGATTGACGTGAGGGG 3955
4014 GCTCCCCCGCGCTTCATAGATGAGTGAAGAGGCTGTGGGATTGACGTGAGGGG 3955

Cy 61 CAGGGATGGCTATA-TTCTGGAGCGAACTCCGGCGAATACGAAGCGCTTGATACGT 119
Db 3954 CAGGGATGGCTATAATTCTCTGGAGCGAACTCCGGCGAATATGAGCGATGATACAG 3955

Cy 120 TGTAGGAGGGATT 133
Db 3894 TTAGCCTTGGAAT 3881

RESULT 11
US-10-680-824A-1/c
Sequence 1, Application US/10680824A
Publication No. US2004013937A1
GENERAL INFORMATION:
APPLICANT: Boudreau, Eric
APPLICANT: Gu, Weining
APPLICANT: De Fremont, Anic
APPLICANT: Helfetz, Peter
TITLE OF INVENTION: Placid Transformation
FILE REFERENCE: 70149USNP
CURRENT APPLICATION NUMBER: US/10/680,824A
PRIOR FILING DATE: 2003-10-07
PRIORITY APPLICATION NUMBER: 60/418596
PRIOR FILING DATE: 2002-07-10
NUMBER OF SEQ ID NOS: 29
SOFTWARE: Patentin version 3.1
SEQ ID NO 1
LENGTH: 7652
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURES:
OTHER INFORMATION: pEBPOT plasmid transformation vector (Example 1 VII).
US-10-680-824A-1

Query Match 77.3%; Score 102.8; DB 7; Length 7652;
Best Local Similarity 90.3%; Pred. No. 6,9e-28;
Matches 121; Conservative 0; Mismatches 12; Indels 1; Gaps 1;

Cy 1 GCTCCCCCGCGCTTCATAGATGAGTGAAGAGGCTGTGGGATTGACGTGAGGGG 60
Db 6644 GCTCCCCCGCGCTTCATAGATGAGTGAAGAGGCTGTGGGATTGACGTGAGGGG 6585
6644 GCTCCCCCGCGCTTCATAGATGAGTGAAGAGGCTGTGGGATTGACGTGAGGGG 6585

Cy 61 CAGGGATGGCTATA-TTCTGGAGCGAACTCCGGCGAATACGAAGCGCTTGATACGT 119
Db 6584 CAGGGATGGCTATAATTCTCTGGAGCGAACTCCGGCGAATATGAGCGCATGATACAG 6525

Cy 120 TGTAGGAGGGATT 133
Db 6525 TGTAGGAGGGATT 133

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Matches 121; Conservative 0; Mismatches 12; Indels 1; Gaps 1;

; PRIOR FILING DATE: 2002-07-10
 ; NUMBER OF SEQ ID NOS: 29

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/ SOFTWARE: Patentin version 3.1
/ SEQ ID NO 2
/ LENGTH: 8684
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: pEB8 (= pEB8a) plasmid transformation vector (Example 2).
US-10-680-824A-2
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Query Match          72.3%; Score 96.2; DB 7; Length 8684;
Best Local Similarity 95.3%; Pred. No. 2.1e-25;
Matches 121; Conservative 0; Mismatches 3; Indels 3; Gaps 2;
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QY      8 CGCCGTCGTTCAATGAGATGATAAGAGGCTCGTGGAATTGACGTAGAGGCGCAGGAT 67
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DB      506 CGCCGTCGTTCAATGAGATGATAAGAGGCTCGTGGAATTGACGTAGAGGCGCAGGAT 447
QY      68 GGCCTATA-TTCTGGAGACCACTCCGGGCGAATACGAGCGCTTGGATACAGTTGTAGG 126
        |||||||
DB      446 GGCCTATATTCTGGAGACCACTCCGGGCGAATACGAGCGCTTGGAT--AGTTGTAGG 389
QY      127 AGGGATT 133
        |||||||
DB      388 AGGGATT 382
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Search completed: April 17, 2006, 23:57:07
Job time : 455 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceeleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 17, 2006, 23:46:06 ; Search time 148 Seconds
(without alignments)
1597.403 Million cell updates/sec

Title: US-10-663-241-32

Perfect score: 133
Sequence: 1 gctcccccgcgtctcaaa.....taccgttctaggaaggatt 133

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_MA.*
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2: /cgn2_6/ptodata/1/ina/5.COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A.COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B.COMB.seq:*
5: /cgn2_6/ptodata/1/ina/H.COMB.seq:*
6: /cgn2_6/ptodata/1/ina/PCTUS.COMB.seq:*
7: /cgn2_6/ptodata/1/ina/PP.COMB.seq:*
8: /cgn2_6/ptodata/1/ina/RB.COMB.seq:*
9: /cgn2_6/ptodata/1/ina/backfillseq.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	133	100.0	133	3	US-09-445-283C-32
2	122	91.7	165	3	US-08-189-256A-4
3	122	91.7	165	3	US-09-193-853-4
4	122	91.7	168	2	US-08-189-256A-2
5	122	91.7	168	3	US-09-193-853-2
6	122	91.7	1134	2	US-08-189-256A-10
7	122	91.7	1134	3	US-09-193-853-10
8	122	91.7	1143	3	US-09-142-114B-6
9	122	91.7	1416	2	US-08-189-256A-27
10	122	91.7	1416	3	US-09-193-853-27
11	122	91.7	1417	3	US-09-142-114B-7
12	121	91.0	161	2	US-08-189-256A-18
13	121	91.0	161	3	US-09-193-853-18
14	121	91.0	300	3	US-09-202-316-4
15	121	91.0	300	3	US-09-202-316-7
16	121	91.0	1208	3	US-08-189-256A-28
17	121	91.0	1208	3	US-09-193-853-28
18	118.8	89.3	150	2	US-08-189-256A-1
19	118.8	89.3	150	3	US-09-193-853-1
20	102.8	77.3	184	3	US-09-283-419-3
21	102.8	77.3	201	3	US-09-011-336-58
22	102.8	77.3	2962	2	US-08-189-256A-3
23	102.8	77.3	2962	3	US-09-193-853-3
24	102.8	77.3	6477	3	US-09-936-588-63

25	99.8	75.0	127	3	US-09-635-132-16	Sequence 16, Appl
26	88.8	66.8	164	2	US-08-189-256A-26	Sequence 26, Appl
27	88.8	66.8	164	3	US-09-193-853-26	Sequence 26, Appl
28	88.4	66.5	129	2	US-08-189-256A-25	Sequence 25, Appl
29	88.4	66.5	129	3	US-09-193-853-25	Sequence 25, Appl
30	88.4	66.5	140	2	US-08-189-256A-19	Sequence 19, Appl
31	88.4	66.5	140	3	US-09-193-853-19	Sequence 19, Appl
32	88	66.2	168	3	US-09-351-123-5	Sequence 5, Appl
33	88	66.2	258	2	US-08-189-256A-24	Sequence 24, Appl
34	88	66.2	258	3	US-09-193-853-24	Sequence 24, Appl
35	87.4	65.7	202	3	US-09-843-324A-1	Sequence 1, Appl
36	87.4	65.7	244	3	US-09-351-123-6	Sequence 6, Appl
37	87.4	65.7	244	3	US-09-843-324A-2	Sequence 2, Appl
38	83.6	62.9	369	3	US-09-265-919-10	Sequence 10, Appl
39	83.6	62.9	1993	3	US-09-142-114B-5	Sequence 5, Appl
40	83.6	62.9	7455	3	US-10-220-557-19	Sequence 19, Appl
41	83.6	62.9	7455	3	US-10-219-227-19	Sequence 19, Appl
42	82.6	62.1	117	2	US-08-217-360-14	Sequence 14, Appl
43	79.8	60.0	139	2	US-08-217-360-13	Sequence 13, Appl
44	77.2	58.0	146	2	US-08-217-360-17	Sequence 17, Appl
45	77.2	58.0	171	2	US-08-217-360-16	Sequence 16, Appl

ALIGNMENTS

RESULT 1
US-09-445-283C-32
Sequence 32, Application US/09445283C
Patent No. 6624296
GENERAL INFORMATION:
APPLICANT: Malliga, Pal
APPLICANT: Silhavy, Daniel
APPLICANT: Striman, Priya
TITLE OR INVENTION: Placid Promoters for Transgene
FILE REFERENCE: RUC 97-0097
CURRENT APPLICATION NUMBER: US/09-445,283C
PRIOR FILING DATE: 1999-12-03
PRIOR APPLICATION NUMBER: PCT/US98/11437
PRIOR FILING DATE: 1998-06-03
PRIOR APPLICATION NUMBER: 60/058,670
PRIOR FILING DATE: 1997-09-12
PRIOR APPLICATION NUMBER: 60/048,376
PRIOR FILING DATE: 1997-06-03
NUMBER OF SEQ ID NOS: 64
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 32
LENGTH: 133
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Prrn promoter
US-09-445-283C-32

Query Match 100.0%; Score 133; DB 3; Length 133;
Best Local Similarity 100.0%; Pred. No. 4,5e-39;
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCCCCCGCGTTCATGAGATGAAGAGGCTGTGATGACGTGAGGGG 60
1 GCTCCCCCGCGTTCATGAGATGAAGAGGCTGTGATGACGTGAGGGG 60
Db CAGGATGCTATATTCGTGAGACCAATCCGGCCGAATTCGAAGCGCTTGATCAGTT 120
61 CAGGATGCTATATTCGTGAGACCAATCCGGCCGAATTCGAAGCGCTTGATCAGTT 120
QY 121 GTAGGAGGAGATT 133
121 GTAGGAGGAGATT 133
Db 121 GTAGGAGGAGATT 133

RESULT 2

US-08-189-256A-4
Sequence 4, Application US/08189256A
Patent No. 5877402
GENERAL INFORMATION:
APPLICANT: Maliga, Pal
APPLICANT: Svab, Zora
APPLICANT: Staud, Jeffrey
APPLICANT: Zoubenko, Oleg V.
APPLICANT: Allison, Lori A.
APPLICANT: Carrier, Helaine
TITLE OF INVENTION: DNA Constructs and Methods for Stably
TITLE OF INVENTION: Transforming Plasmids of Multicellular Plants and
TITLE OF INVENTION: Expressing Recombinant Proteins Therein
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Dann, Dorfman, Herrell and Skillman
STREET: 1601 Market Street Suite 720
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103-2307
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/189,256A
FILING DATE: 31-JAN-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/111,398
FILING DATE: 25-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/518,763
FILING DATE: 01-MAY-1990
ATTORNEY/AGENT INFORMATION:
NAME: Reed, Janet E.
REGISTRATION NUMBER: 36,252
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 563-4100
TELEFAX: (215) 563-4044
INFORMATION FOR SEQ ID NO.: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 165 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-189-256A-4

	Query Match	91.7%	Score 122;	DB 2;	Length 165;
	Best Local Similarity	99.3%;	Pred.	No.5.2e-35;	
	Matches 133; Conservative	0;	Mismatches	0;	Indels 1; Gaps 1.
Oy	1	GCTCCCCCGCGTCGTTCAATGAGAATGAGTGAAGGCGTCGTGGATTGACGTGAGGGGG	60		
Dd	1	GCTCCCCCGCGTCGTTCAATGAGAATGAGTGAAGGCGTCGTGGATTGACGTGAGGGGG	60		
Oy	61	CAGGAGATGGCTATA-TTCTGGAGGCGAACTCCGGCGMAATACGAAGCGTTGGATACAGT	119		
Dd	61	CAGGAGATGGCTATAATTCTGGAGGCGAACTCCGGCGMAATACGAAGCGCTTGATACAGT	120		
Oy	120	TGTAGGAGGAGGATT	133		
Dd	121	TGTAGGAGGAGGATT	134		
RESULT 3					
	US-09-193-853-4				

Sequence 4 Application US/09193853
Patent No. 6388168
GENERAL INFORMATION:
APPLICANT: Maligna, Pal
APPLICANT: Svab, Zora
APPLICANT: Staub, Jeffrey
APPLICANT: Zoubenko, Oleg V.
APPLICANT: Allison, Lori A.
APPLICANT: Carver, Helaine
APPLICANT: Kanevski, Ivan
TITLE OF INVENTION: DNA Constructs and Methods for Stably
TITLE OF INVENTION: Transforming Plasmids of Multicellular Plants and
TITLE OF INVENTION: Expressing Recombinant Proteins Therein
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dann, Dorfman, Herrell and Skillman
STREET: 1601 Market Street Suite 720
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103-2307
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/193,853
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/189,256
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/518,763
FILING DATE: 01-MAY-1990
ATTORNEY/AGENT INFORMATION:
NAME: Reed, Janet E.
REGISTRATION NUMBER: 36,252
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 563-4100
TELEFAX: (215) 563-4044
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 165 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-09-193-853-4

	Query Match	91.7%	Score 122;	DB 3;	Length 165;
	Best Local Similarity	99.3%	Pred. No. 5.2e-35;		
	Matches 133;	Conservative 0;	Mismatches 0;	Indels 1;	Gaps 1
Qy	1	GCTCCCCCGCCGTCGTCGATGAGATGATGAAGAGGCTCGTGGATTGACCTGAGGGG	60		
Db	1	GCTCCCCCGCCGTCGTCGATGAGATGAGATGAGGCTCGTGGATTGACCTGAGGGG	60		
Qy	61	CAGGGATGCGCTATA-TTCTGGGAGCGAACTCCGGCGGATACGAAGCGCTTGATACAGT	119		
Db	61	CAGGGATGCGCTATA-TTCTGGGAGCGAACTCCGGCGGATACGAAGCGCTTGATACAGT	120		
Qy	120	TGTAGGAGGGGATT	133		
Db	121	TGTAGGAGGGGATT	134		

RESULT 4
US-08-189-256A-2
; Sequence 2, Application US/08189256A

Patent No. 5877402
GENERAL INFORMATION:
APPLICANT: Maliga, Pal
APPLICANT: Svab, Zora
APPLICANT: Staud, Jeffrey
APPLICANT: Zoubenko, Oleg V.
APPLICANT: Allison, Lori A.
APPLICANT: Carreer, Helaine
APPLICANT: Kanevsk, Ivan
TITLE OF INVENTION: DNA Constructs and Methods for Stably
Transforming Plasmids of Multicellular Plants and
Expressing Recombinant Proteins Therein
TITLE OF INVENTION: Transforming Plasmids of Multicellular Plants and
Expressing Recombinant Proteins Therein
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dann, Dorfman, Herrell and Skillman
STREET: 1601 Market Street Suite 720
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103-2307
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/189,256A
FILING DATE: 31-JAN-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/111,398
FILING DATE: 25-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/518,763
FILING DATE: 01-MAY-1990
ATTORNEY/AGENT INFORMATION:
NAME: Reed, Janet E.
REGISTRATION NUMBER: 36,252
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 563-4100
TELEFAX: (215) 563-4044
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 168 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: not relevant
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-189-256A-2

Query Match 91.7%; Score 122; DB 2; Length 168;
Best Local Similarity 99.3%; Pred. No. 5.2e-35;
Matches 133; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1 GCTCCCCCGCGCTGTTCAATGAGATGATTAAGAGCTGTTGGATTGACGAGGGGG 60
DB 1 GCTCCCCCGCGCTGTTCAATGAGATGATTAAGAGCTGTTGGATTGACGAGGGGG 60
QY 61 CAGGATGGCTATA-TTCTGGAGCGAATCTCCGGCGAATACGAAGCGCTTGATACAGT 119
DB 61 CAGGATGGCTATA-TTCTGGAGCGAATCTCCGGCGAATACGAAGCGCTTGATACAGT 120
QY 120 TGTAGGAGGAGATT 133
DB 121 TGTAGGAGGAGATT 134

RESULT 5
US-09-193-853-2
Sequence 2, Application US/09193853
Patent No. 6386168

GENERAL INFORMATION:
APPLICANT: Maliga, Pal
APPLICANT: Svab, Zora
APPLICANT: Staud, Jeffrey
APPLICANT: Zoubenko, Oleg V.
APPLICANT: Allison, Lori A.
APPLICANT: Carreer, Helaine
APPLICANT: Kanevsk, Ivan
TITLE OF INVENTION: DNA Constructs and Methods for Stably
Transforming Plasmids of Multicellular Plants and
Expressing Recombinant Proteins Therein
TITLE OF INVENTION: Transforming Plasmids of Multicellular Plants and
Expressing Recombinant Proteins Therein
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dann, Dorfman, Herrell and Skillman
STREET: 1601 Market Street Suite 720
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103-2307
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/193,853
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/189,256
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/518,763
FILING DATE: 01-MAY-1990
ATTORNEY/AGENT INFORMATION:
NAME: Reed, Janet E.
REGISTRATION NUMBER: 36,252
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 563-4100
TELEFAX: (215) 563-4044
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 168 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: not relevant
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-09-193-853-2

Query Match 91.7%; Score 122; DB 3; Length 168;
Best Local Similarity 99.3%; Pred. No. 5.2e-35;
Matches 133; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1 GCTCCCCCGCGCTGTTCAATGAGATGATTAAGAGCTGTTGGATTGACGAGGGGG 60
DB 1 GCTCCCCCGCGCTGTTCAATGAGATGATTAAGAGCTGTTGGATTGACGAGGGGG 60
QY 61 CAGGATGGCTATA-TTCTGGAGCGAATCTCCGGCGAATACGAAGCGCTTGATACAGT 119
DB 61 CAGGATGGCTATA-TTCTGGAGCGAATCTCCGGCGAATACGAAGCGCTTGATACAGT 120
QY 120 TGTAGGAGGAGATT 133
DB 121 TGTAGGAGGAGATT 134

RESULT 6
US-08-189-256A-10/c
Sequence 10, Application US/08189256A
Patent No. 5877402
GENERAL INFORMATION:

```

; APPLICANT: Maliga, Pal
; APPLICANT: Svab, Zora
; APPLICANT: Straub, Jeffrey
; APPLICANT: Zoubenko, Oleg V.
; APPLICANT: Allison, Lori A.
; APPLICANT: Carter, Helaine
; APPLICANT: Kanevski, Ivan
; TITLE OF INVENTION: DNA Constructs and Methods for Stably
; TITLE OF INVENTION: Transforming Plasmids of Multicellular Plants and
; TITLE OF INVENTION: Expressing Recombinant Proteins Therein
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dann, Dorfman, Herrell and Skillman
; STREET: 1601 Market Street Suite 720
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103-2307
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/189,256A
; FILING DATE: 31-JAN-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/111,398
; FILING DATE: 25-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/518,763
; FILING DATE: 01-MAY-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Reed, Janet E.
; REGISTRATION NUMBER: 36,252
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 563-4100
; TELEFAX: (215) 563-4044
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1134 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; US-08-189-256A-10
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Query Match          91.7%; Score 122; DB 2; Length 1134;
Best Local Similarity 99.3%; Pred. No. 1e-34;
Matches 133; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 GCTCCCCCGCGTCTTCAATGAGATGAAGAGAGCTTGTGGATTGACGTGAGGGGG 60
DB 1058 GCTCCCCCGCGTCTTCAATGAGATGAAGAGAGCTTGTGGATTGACGTGAGGGGG 999

QY 61 CAGGATGAGCTATA-TTCTGGAGAGCACTCCGGGCGAATACGAACGCTTGATACAGT 119
DB 998 CAGGATGAGCTATA-TTCTGGAGAGCACTCCGGGCGAATACGAACGCTTGATACAGT 939

QY 120 TGTAGGAGGAGATT 133
DB 938 TGTAGGAGGAGATT 925
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RESULT 7
US-09-193-853-10/c
; Sequence 10, Application US/09193853
; Patent No. 6388168
; GENERAL INFORMATION:
; APPLICANT: Maliga, Pal
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```

; APPLICANT: Svab, Zora
; APPLICANT: Straub, Jeffrey
; APPLICANT: Zoubenko, Oleg V.
; APPLICANT: Allison, Lori A.
; APPLICANT: Carter, Helaine
; APPLICANT: Kanevski, Ivan
; TITLE OF INVENTION: DNA Constructs and Methods for Stably
; TITLE OF INVENTION: Transforming Plasmids of Multicellular Plants and
; TITLE OF INVENTION: Expressing Recombinant Proteins Therein
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dann, Dorfman, Herrell and Skillman
; STREET: 1601 Market Street Suite 720
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103-2307
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/193,853
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/189,256
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/518,763
; FILING DATE: 01-MAY-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Reed, Janet E.
; REGISTRATION NUMBER: 36,252
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 563-4100
; TELEFAX: (215) 563-4044
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1134 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; US-09-193-853-10
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Query Match          91.7%; Score 122; DB 3; Length 1134;
Best Local Similarity 99.3%; Pred. No. 1e-34;
Matches 133; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 GCTCCCCCGCGTCTTCAATGAGATGAAGAGAGCTTGTGGATTGACGTGAGGGGG 60
DB 1058 GCTCCCCCGCGTCTTCAATGAGATGAAGAGAGCTTGTGGATTGACGTGAGGGGG 999

QY 61 CAGGATGAGCTATA-TTCTGGAGAGCACTCCGGGCGAATACGAACGCTTGATACAGT 119
DB 998 CAGGATGAGCTATA-TTCTGGAGAGCACTCCGGGCGAATACGAACGCTTGATACAGT 939

QY 120 TGTAGGAGGAGATT 133
DB 938 TGTAGGAGGAGATT 925
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```

RESULT 8
US-09-142-114B-6/c
; Sequence 6, Application US/09142114B
; Patent No. 6376744
; GENERAL INFORMATION:
; APPLICANT: Rutgers University
; APPLICANT: Maliga, Pal
```


APPLICATION NUMBER: US 01/518,763
FILING DATE: 01-MAY-1990
ATTORNEY/AGENT INFORMATION:

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;
; ATTORNEY/AGENT INFORMATION:
; NAME: Reed, Janet E.

```

REGISTRATION NUMBER: 36,252
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 563-4100
TELEFAX: (215) 563-4044
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 1416 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-09-193-853-27

Query Match 91.7%; Score 122; DB 3; Length 1416;
Best Local Similarity 99.3%; Pred. No. 1.1e-34;
Matches 133; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 GCTCCCCCGCGCTGTTCAATGAGATGAGATGAGAGGCTGTTGAGTTGACGTGAGGGG 60
DB 22 GCTCCCCCGCGCTGTTCAATGAGATGAGATGAGAGGCTGTTGAGTTGACGTGAGGGG 81
QY 61 CAGGGATGGCTATA-TTCTGGAGGCGAACTCCGGGCGAATACGAAGCGCTTGATACAGT 119
DB 82 CAGGGATGGCTATAATTCTGGAGCGAACTCCGGGCGAATACGAAGCGCTTGATACAGT 141
QY 120 TGTAGGAGGGGATT 133
DB 142 TGTAGGAGGGGATT 155

RESULT 11

US-09-142-114B-7
Sequence 7, Application US/09142114B
Patent No. 6376744
GENERAL INFORMATION:
APPLICANT: Rutgers University
APPLICANT: Malliga, Pal
APPLICANT: Sikdar, Samir R.
APPLICANT: Reddy, Siva Ranga
TITLE OF INVENTION: Placitid Transformation in Arabidopsis
TITLE OF INVENTION: Thailana
FILE REFERENCE: 09/142,114
CURRENT APPLICATION NUMBER: US/09/142,114B
CURRENT FILING DATE: 1999-02-05
PRIOR APPLICATION NUMBER: PCT/US97/03444
PRIOR FILING DATE: 1997-03-06
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 7
LENGTH: 1417
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Sequence source:/note="synthetic construct"
Patent No. 6376744
US-09-142-114B-7

Query Match 91.7%; Score 122; DB 3; Length 1417;
Best Local Similarity 99.3%; Pred. No. 1.1e-34;
Matches 133; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 GCTCCCCCGCGCTGTTCAATGAGATGAGATGAGAGGCTGTTGAGTTGACGTGAGGGG 60
DB 23 GCTCCCCCGCGCTGTTCAATGAGATGAGATGAGAGGCTGTTGAGTTGACGTGAGGGG 82
QY 61 CAGGGATGGCTATA-TTCTGGAGGCGAACTCCGGGCGAATACGAAGCGCTTGATACAGT 119
DB 83 CAGGGATGGCTATAATTCTGGAGCGAACTCCGGGCGAATACGAAGCGCTTGATACAGT 142
QY 120 TGTAGGAGGGGATT 133
DB 142 TGTAGGAGGGGATT 155

DB 143 TGTAGGAGGGGATT 156

RESULT 12
US-08-189-256A-18
Sequence 18, Application US/08189256A
Patent No. 5877402
GENERAL INFORMATION:
APPLICANT: Malliga, Pal
APPLICANT: Svab, Zora
APPLICANT: Steub, Jeffrey
APPLICANT: Zoubenko, Oleg V.
APPLICANT: Allison, Lori A.
APPLICANT: Carrier, Helaine
APPLICANT: Kanevski, Ivan
TITLE OF INVENTION: DNA Constructs and Methods for Stably
TITLE OF INVENTION: Transforming Placitids of Multicellular Plants and
TITLE OF INVENTION: Expressing Recombinant Proteins Therein
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSER: Dann, Dorfman, Herrell and Skillman
STREET: 1601 Market Street Suite 720
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103-2307
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/189,256A
FILING DATE: 31-JAN-1994
CLASSIFICATION: A35
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/111,398
FILING DATE: 25-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/518,763
FILING DATE: 01-MAY-1990
ATTORNEY/AGENT INFORMATION:
NAME: Reed, Janet E.
REGISTRATION NUMBER: 36,252
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 563-4100
TELEFAX: (215) 563-4044
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 161 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-189-256A-18

Query Match 91.0%; Score 121; DB 2; Length 161;
Best Local Similarity 99.2%; Pred. No. 1.2e-34;
Matches 132; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 GCTCCCCCGCGCTGTTCAATGAGATGAGATGAGAGGCTGTTGAGTTGACGTGAGGGG 60
DB 23 GCTCCCCCGCGCTGTTCAATGAGATGAGATGAGAGGCTGTTGAGTTGACGTGAGGGG 82
QY 61 CAGGGATGGCTATA-TTCTGGAGGCGAACTCCGGGCGAATACGAAGCGCTTGATACAGT 119
DB 83 CAGGGATGGCTATAATTCTGGAGCGAACTCCGGGCGAATACGAAGCGCTTGATACAGT 142
QY 120 TGTAGGAGGGGATT 132
DB 143 TGTAGGAGGGGATT 155

RESULT 13
US-09-193-853-18
Sequence 18, Application US/09193853
Patent No. 6388168
GENERAL INFORMATION:
APPLICANT: Maliga, Pal
APPLICANT: Svab, Zora
APPLICANT: Staub, Jeffrey
APPLICANT: Zoubenko, Oleg V.
APPLICANT: Allison, Lori A.
APPLICANT: Carreir, Helaine
APPLICANT: Kanevski, Ivan
TITLE OF INVENTION: DNA Constructs and Methods for Stably
TITLE OF INVENTION: Transforming Plasmids of Multicellular Plants and
TITLE OF INVENTION: Expressing Recombinant Proteins Therein
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dann, Dorfman, Herrell and Skillman
STREET: 1601 Market Street Suite 720
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103-2307
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/193,853
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/189,256
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/518,763
FILING DATE: 01-MAY-1990
ATTORNEY/AGENT INFORMATION:
NAME: Reed, Janet E.
REGISTRATION NUMBER: 36,252
TELEPHONE: (215) 563-4100
TELEFAX: (215) 563-4044
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 161 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-09-193-853-18

Query Match 91.0%; Score 121; DB 3; Length 161;
Best Local Similarity 99.2%; Pred. No. 1.2e-34;
Matches 132; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 GCTCCCCCGCGTTCATGAGATGATAGAGGCTCGTGGATTGACGTAGGGG 60
DB 23 GCTCCCCCGCGTTCATGAGATGATAGAGGCTCGTGGATTGACGTAGGGG 82

QY 61 CAGGATGGCTATA-TTCTGGAGCGAATCTCGGCGCAATACGAAGCGCTTGATACAGT 119
DB 83 CAGGATGGCTATAATTCTGGAGCGAATCTCGGCGCAATACGAAGCGCTTGATACAGT 142

QY 120 TGTAGGAGGAGAT 132
DB 143 TGTAGGAGGAGAT 155

RESULT 14
US-09-202-316-4
Sequence 4, Application US/09202316
Patent No. 6297054
GENERAL INFORMATION:
APPLICANT: Pal Maliga
APPLICANT: Helaine Carreir
APPLICANT: Sumita Chaudhuri
TITLE OF INVENTION: Editing-Based Selectable Plasmid Marker
TITLE OF INVENTION: Genes
FILE REFERENCE: Rut-96-06041
CURRENT APPLICATION NUMBER: US/09/202,316
PRIOR FILING DATE: 1999-06-01
PRIOR APPLICATION NUMBER: PCT/US97/10318
PRIOR FILING DATE: 1997-06-13
PRIOR APPLICATION NUMBER: 60/019,741
PRIOR FILING DATE: 1996-06-14
NUMBER OF SEQ ID NOS: 60
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 4
LENGTH: 300
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic Sequence
US-09-202-316-4

Query Match 91.0%; Score 121; DB 3; Length 300;
Best Local Similarity 99.2%; Pred. No. 1.5e-34;
Matches 132; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 GCTCCCCCGCGTTCATGAGATGATAGAGGCTCGTGGATTGACGTAGGGG 60
DB 17 GCTCCCCCGCGTTCATGAGATGATAGAGGCTCGTGGATTGACGTAGGGG 76

QY 61 CAGGATGGCTATA-TTCTGGAGCGAATCTCGGCGCAATACGAAGCGCTTGATACAGT 119
DB 77 CAGGATGGCTATAATTCTGGAGCGAATCTCGGCGCAATACGAAGCGCTTGATACAGT 136

QY 120 TGTAGGAGGAGAT 132
DB 137 TGTAGGAGGAGAT 149

RESULT 15
US-09-202-316-7
Sequence 7, Application US/09202316
Patent No. 6297054
GENERAL INFORMATION:
APPLICANT: Pal Maliga
APPLICANT: Helaine Carreir
APPLICANT: Sumita Chaudhuri
TITLE OF INVENTION: Editing-Based Selectable Plasmid Marker
TITLE OF INVENTION: Genes
FILE REFERENCE: Rut-96-06041
CURRENT APPLICATION NUMBER: US/09/202,316
PRIOR FILING DATE: 1999-06-01
PRIOR APPLICATION NUMBER: PCT/US97/10318
PRIOR FILING DATE: 1997-06-13
PRIOR APPLICATION NUMBER: 60/019,741
PRIOR FILING DATE: 1996-06-14
NUMBER OF SEQ ID NOS: 60
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 7
LENGTH: 300
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic Sequence
US-09-202-316-7

Query Match 91.0%; Score 121; DB 3; Length 300;

Best Local Similarity 99.2%; Pred. No. 1.5e-34;
Matches 132; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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Qy 1 GCTCCCCCGCGTTCATATGAGATGATTAAGAGCGCTCGTGGATTGACGTAGGGGG 60
    |||||||
Db 17 GCTCCCCCGCGCGTTCATATGAGATGATTAAGAGCGCTCGTGGATTGACGTAGGGGG 76
    |||||||
Qy 61 CAGGATGGCTATA-TTCTGGAGCGGACTCCGGCGAATACGAGCGCTTGGATACAGT 119
    |||||||
Db 77 CAGGATGGCTATTTCTGGAGCGGACTCCGGCGAATACGAGCGCTTGGATACAGT 136
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Qy 120 TGTAGGAGAGGAT 132
    |||||||
Db 137 TGTAGGAGAGGAT 149
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Search completed: April 18, 2006, 00:25:54
Job time : 149 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 17, 2006, 23:45:48 ; Search time 2980 Seconds
(without alignments)
2088.148 Million cell updates/sec

Title: US-10-663-241-32

Perfect score: 133
Sequence: 1 gctcccccgcgcgtctcaaa.....tacagttcgtagggaggtac 133

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 41078325 segs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST: *
1: gb_est1.*
2: gb_est2.*
3: gb_est3.*
4: gb_hnc.*
5: gb_est4.*
6: gb_est5.*
7: gb_est6.*
8: gb_est7.*
9: gb_gss1.*
10: gb_gss2.*
11: gb_gss3.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	92.2	69.3	734	10	CG026772 PBAAB74TR
2	91.6	68.9	415	7	CN930271 000322AFB
3	91.6	68.9	498	7	CN872595 020807AAP
4	91.6	68.9	510	1	AJ876197 AJ876197
5	91.6	68.9	598	7	CN871707 010128AAP
6	91.6	68.9	763	9	BH515735 BOKKC79TR
7	91.6	68.9	764	10	CG026604 PBAAB30TR
8	91.2	68.6	610	7	CK767400 pamt1-9ms
9	91.1	68.4	839	9	BH674012 BOMHD96TR
10	90.6	68.1	380	7	CN859023 000728AAA
11	85.4	64.2	491	9	BH009864 eg27202.x
12	85.2	64.1	770	9	BZ511771 BOMCOT2TR
13	85.2	64.1	775	9	BH424823 BOMN79TR
14	84.2	63.3	713	9	BH957918 odt85c05.
15	83.6	62.9	183	9	BZ483881 BOCAL29TR
16	83.6	62.9	199	9	BH537952 BOCGFU8TR
17	83.6	62.9	238	9	BH677595 BOCMA9TR
18	83.6	62.9	292	9	BH474703 BOCG149TF
19	83.6	62.9	322	9	BH705426 BOMAG13TR
20	83.6	62.9	326	9	BZ440851 BOMN37TR
21	83.6	62.9	337	9	BZ464817 BOMC007TR
22	83.6	62.9	361	9	BZ470963 BOMB24TR

23	83.6	62.9	367	9	BH430502	BH430502
24	83.6	62.9	368	9	BH493122	BH493122
25	83.6	62.9	407	9	BZ489878	BZ489878
26	83.6	62.9	416	9	BH664090	BH664090
27	83.6	62.9	419	9	BH662193	BH662193
28	83.6	62.9	422	9	BH475597	BH475597
29	83.6	62.9	423	9	BH653681	BH653681
30	83.6	62.9	434	9	BH545732	BH545732
31	83.6	62.9	434	9	BH678091	BH678091
32	83.6	62.9	435	9	BZ447238	BZ447238
33	83.6	62.9	441	9	BH657205	BH657205
34	83.6	62.9	441	9	CC966698	CC966698
35	83.6	62.9	448	9	BH689289	BH689289
36	83.6	62.9	450	9	BH725279	BH725279
37	83.6	62.9	451	9	BH719545	BH719545
38	83.6	62.9	459	9	BH562132	BH562132
39	83.6	62.9	466	9	BH541747	BH541747
40	83.6	62.9	468	9	BH740372	BH740372
41	83.6	62.9	469	9	BH718684	BH718684
42	83.6	62.9	475	9	BH669610	BH669610
43	83.6	62.9	475	9	BH700638	BH700638
44	83.6	62.9	482	9	BH649351	BH649351
45	83.6	62.9	484	9	BH650341	BH650341

ALIGNMENTS

RESULT 1
CG026772/c 734 bp DNA linear GSS 19-AUG-2003
LOCUS PBAAB74TR
DEFINITION PGAB74TR Carica papaya genomic clone PBAAB74, genomic survey
ACCESSION CG026772
VERSION CG026772.1 GI:338982928
KEYWORDS GSS.
SOURCE Carica papaya (papaya)
ORGANISM Carica papaya

REFERENCE
AUTHORS Town, C.D., Van Aken, S., Ulteback, T., and Fraser, C.M.
TITLE Whole genome shotgun sequencing of Carica papaya
JOURNAL Unpublished (2003)
COMMENT Other_GSSs: PBAAB74TF
Contact: Chris Town
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208

FEATURES
source
Email: cdtown@tigr.org
DNA provided by Ray King was isolated from cultivar SunUp that was
transgenic for papaya ringspot virus coat protein gene
Seq primer: TR
Class: sheared ends.
location/Qualifiers
1..734
/organism="Carica papaya"
/mol_type="genomic DNA"
/cultivar="SunUp"
/db_xref="taxon:3649"
/clone_lib="PBAAB74"
/clone_lib="PBAAB74"
/note="Vector: pBOS1, Site 1: BstXI, 2-3 kb sheared
genomic DNA inserted into pBOS1 using BstXI linkers"

ORIGIN

Query Match 69.3%; Score 92.2; DB 10; Length 734;
Best Local Similarity 85.7%; Pred. No. 4.2e-19;
Matches 114; Conservative 0; Mismatches 18; Indels 1; Gaps 1;
QY 1 GCTCCCGCGCGTGTTCATGAGATGAGATGAGAGGCTGTGAGATTGACGTAGAGGGG 60

Db	LOCUS	DEFINITION	ACCESSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT	FEATURES	ORIGIN
Dp	154	GCTCCCCCGCGTATCGAATTAAGATGATTAAGAGCTCGTGGATTGACGTAGGGGG											
Qy	61	CAGGATATGGCTATA-TTCTGGAGCGAATCCGGCGAATACGAAGCGCTTGATACGT	119										
Dp	94	TAGGATATGGCTATA-TTCTGGAGCGAATCCGGCGAATACGAAGCGCTTGATACGT	35										
Qy	120	TGTAGGAGGGAT	132										
Dp	34	TTATGCTTGGAAT	22										
RESULT 2													
LOCUS	CN930271	415 bp	mRNA	linear	EST 07-JUN-2004								
DEFINITION	000322AFBC002396HT (AFBC) Royal Gala pre-opened floral bud Malus x domestica cDNA AFBC002396, mRNA sequence.												
ACCESSION	CN930271												
KEYWORDS	CN930271.1 GI:48403084												
SOURCE	EST.												
ORGANISM	Malus x domestica												
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids 1; Rosales; Rosaceae; Maloideae; Malus.												
AUTHORS	1 (bases 1 to 415) Benning, L., Bowen, J., Crowhurst, R., Gleave, A., Janssen, B., McArtney, S., Newcomb, R., Ross, G., Snowden, K., Walton, E. and Yaak, Y.												
TITLE	HortResearch Apple EST Project												
JOURNAL	Unpublished (2004)												
COMMENT	Contact: Gleave, A. Sequencing Facility The Horticulture and Food Research Institute of New Zealand Ltd 120 Mt Albert Rd, Mt Albert, Auckland, New Zealand Tel: 00 64 09 815 4200 Fax: 00 64 09 815 4201 Email: est@hortresearch.co.nz.												
FEATURES	Location/Qualifiers												
source	1..415												
	/organism="Malus x domestica"												
	/mol_type="mRNA"												
	/db_xref="taxon:3750"												
	/clone="AFBC002396"												
	/tissue_type="Floral bud"												
	/dev_stage="Pre-opening, flower at stage of nectar/pollen formation"												
	/clone_id="AFBC" Royal Gala pre-opened floral bud"												
	/note="Vector: pBK-CMV; Library sequenced by Genesys Research & Development"												
ORIGIN													
Query Match	68.9%	Score 91.6;	DB 7;	Length 415;									
Best Local Similarity	85.1%	Pred. No. 6	1e-19;										
Matches 114;	Conservative 0;	Mismatches 19;	Indels 1;	Gaps 1;									
Qy	1	GCTCCCCCGCGTTCGTTCAATGAGATGATTAAGAGGCTCGTGGATTGACGTAGGGGG	60										
Dp	196	GCTTCCCGCGCGTATCGAATGAGATGATTAAGAGGCTCGTGGATTGACGTAGGGGG	255										
Qy	61	CAGGATATGGCTATA-TTCTGGAGCGAATCCGGCGAATACGAAGCGCTTGATACGT	119										
Dp	256	TAGGATATGGCTATA-TTCTGGAGCGAATCCGGCGAATACGAAGCGCTTGATACGT	315										
Qy	120	TGTAGGAGGGATT	133										
Dp	316	TTATGCTTGGAAT	329										
RESULT 3													
LOCUS	CN872595	498 bp	mRNA	linear	EST 04-JUN-2004								

ACCESSION	CN872595
VERSION	CN872595.1
KEYWORDS	GI:48258753
SOURCE	EST.
ORGANISM	Malus x domestica
TITLE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; euroside 1; Rosales; Rosaceae; Maloideae; Malus.
AUTHORS	Bennings, L., Bowen, J., Crowhurst, R., Gleave, A., Janssen, B., McArtney, S., Newcomb, R., Rose, G., Snowden, K., Walton, E. and Yauk, Y.
JOURNAL	HortResearch Apple EST Project
COMMENT	Unpublished (2004) Contact: Gleave, A. Sequencing Facility The Horticulture and Food Research Institute of New Zealand Ltd 120 Mt Albert Rd, Mt Albert, Auckland, New Zealand Tel: 00 64 09 815 4200 Fax: 00 64 09 815 4201 Email: est@hortresearch.co.nz.
FEATURES	
source	Location/Qualifiers 1..498 /organism="Malus x domestica" /mol_type="mRNA" /db_xref="taxon:3750" /clone="AAPA005328" /tissue_type="Fruit" /dev_stage="24 days after full bloom" /clone_id="(AAPA) Royal Gala 24 DAFB fruit" /note="Vector: pBK-CMV; Library sequenced by Genesis Research & Development"
ORIGIN	
Query Match	68.9%; Score 91.6; DB 7; Length 498;
Best Local Similarity	85.1%; Pred. No. 6.2e-19;
Matches	114; Conservative 0; Mismatches 19; Indels 1; Gaps 1;
OY	1 GCTCCCCCGCCGTCATCAATGAAGATGAAGAGCTCCTGGATTGACTGAGCGG 60 Db 247 GCTTCCCCCGCGTATCGAATGAAGAATGAAGAGGCTCCTGGATTGAGTGAGCGG 306
OY	61 CAGGATGGCATAT-TTCTGGAGAGCAATCCGGGCCAAATCGAAGGCCTGTGATACGT 119
Db	307 TAGGATGGCATATTTCTGGAGAGCAATCCGAGATATGAAGCGCATGATACAG 366
OY	120 TGTAGGAGAGGATT 133
Db	367 TTATGCTTGGAAAT 380
RESULT 4	
AJ876197/c	510 bp mRNA linear EST 17-FEB-2005
LOCUS	AJ876197 Prunus persica fruit mesocarp plus epidermis 80 days after
DEFINITION	bloom Prunus persica cDNA clone PR0213405, mRNA sequence.
ACCESSION	AJ876197
VERSION	AJ876197.1
KEYWORDS	GI:59932682
SOURCE	EST.
ORGANISM	Prunus persica (peach)
TITLE	Prunus persica
AUTHORS	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; euroside 1; Rosales; Rosaceae; Amygdaloideae; Prunus.
REFERENCE	1 (bases 1 to 510) Le Danec, L., Cosson, P., Renaud, C., Garcia, V., Dumoulin, P., Rochan, C., Filippi, G., Laigret, F., Moing, A. and Dirlewanger, E.
JOURNAL	Peach (Prunus persica (L.) Batsch) fruit ESTs from two early development stages
COMMENT	Unpublished (2004) Contact: Le Danec L urefy, Inra, INRA, Centre de Bordeaux BP 81 Villenave d'Ornon Cedex, 33 883, FRANCE.
FEATURES	Location/Qualifiers

source

1. 510

/organism="Prunus persica"

/mol_type="mRNA"

/cultivar="Fantasia"

/db_xref="taxon:3760"

/clone="PR0213A05"

/tissue_type="fruit mesocarp plus epidermis"

/dev_stage="80 days after bloom"

/clone_lib="Prunus persica fruit mesocarp plus epidermis 80 days after bloom"

Query Match 68.9%; Score 91.6; DB 1; Length 510;

Best Local Similarity 85.1%; Pred. No. 6.3e-19;

Matches 114; Conservative 0; Mismatches 19; Indels 1; Gaps 1;

QY 1 GCTCCCCCGCGTTCATGAGATGATAGAGGCTCGTGGATTGACGTAGGGGG 60

DB 302 GCTTCCCGCGTATCGAATGATGATAGAGGCTCGTGGATTGACGTAGGGGG 243

QY 61 CAGGATGAGCTATA-TTCTGGAGAGCACTCCGGCGAATAGCAAGCGCTTGATACAGT 119

DB 242 TAGGATGAGCTATATTCTGGAGAGCACTCCAGCGAATATGAGCGCATGATACAG 183

QY 120 TGTAGGAGGAGATT 133

DB 182 TTATGCTTGGAAAT 169

RESULT 5

LOCUS CN871707 598 bp mRNA linear EST 04-JUN-2004

DEFINITION 010128AAPA001324HT (AAPA) Royal Gala 24 DAFB fruit Malus x domestica cDNA clone AAPA001324, mRNA sequence.

ACCESSION CN871707

VERSION CN871707.1 GI:48257865

KEYWORDS EST.

SOURCE

ORGANISM

Malus x domestica

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids I; Rosales; Rosaceae; Maloideae; Malus.

REFERENCE

1 (bases 1 to 598)

Burnung, J., Bowen, D., Crowhurst, R., Gleave, A., Janssen, B., Martney, S., Newcomb, R., Ross, G., Snowden, K., Walton, E. and Yauk, Y. HortResearch Apple EST Project

Unpublished (2004)

CONTACT: Gleave, A.

Sequencing Facility

The Horticulture and Food Research Institute of New Zealand Ltd

120 Mc Albert Rd, Mc Albert, Auckland, New Zealand

Tel: 00 64 09 815 4200

Fax: 00 64 09 815 4201

Email: est@hortresearch.co.nz.

FEATURES

source

1. 598

Location/Qualifiers

/organism="Malus x domestica"

/mol_type="mRNA"

/db_xref="taxon:3750"

/clone="AAPA001324"

/tissue_type="Fruit"

/dev_stage="24 days after full bloom"

/clone_lib="(AAPA) Royal Gala 24 DAFB fruit"

/note="Vector: PBK-CMV; Library sequenced by Genesis Research & Development"

ORIGIN

Query Match 68.9%; Score 91.6; DB 7; Length 598;

Best Local Similarity 85.1%; Pred. No. 6.4e-19;

Matches 114; Conservative 0; Mismatches 19; Indels 1; Gaps 1;

QY 1 GCTCCCCCGCGTTCATGAGATGATAGAGGCTCGTGGATTGACGTAGGGGG 60

DB 383 GCTTCCCGCGTATCGAATGATGATAGAGGCTCGTGGATTGACGTAGGGGG 442

QY 61 CAGGATGAGCTATA-TTCTGGAGAGCACTCCGGCGAATAGCAAGCGCTTGATACAGT 119

DB 443 TAGGATGAGCTATATTCTGGAGAGCACTCCAGCGAATATGAGCGCATGATACAG 502

QY 120 TGTAGGAGGAGATT 133

DB 503 TTATGCTTGGAAAT 516

RESULT 6

BH515735/c 763 bp DNA linear GSS 13-DEC-2001

LOCUS BOHKT97R BOHK Brassica oleracea genomic clone BOHKT9, genomic survey sequence.

DEFINITION

ACCESSION BH515735

VERSION BH515735.1 GI:17723825

KEYWORDS GSS.

SOURCE

ORGANISM

Brassica oleracea

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

REFERENCE

1 (bases 1 to 763)

Ayale, M., Haas, B.J., Kumar, N., Wu, H., Xiao, Y., Van Aken, S., Utechtack, T.R., Wortman, J.R., White, O.R. and Town, C.D. Whole genome shotgun sequencing of Brassica oleracea and its application to gene discovery and annotation in Arabidopsis Genome Res. 15 (4), 487-495 (2005)

15805490

Other GSSs: BOHKT97F

Contact: Chris Town

TIGR

JOURNAL

PUBMED

9712 Medical Center Drive, Rockville, MD 20850, USA.

Tel: 301-838-3523

Fax: 301-838-0208

Email: cdtown@tigr.org

DNA is from a doubled haploid provided by Tom Osborn.

Seq primer: TR

Class: Sineared ends.

FEATURES

source

1. 763

Location/Qualifiers

/organism="Brassica oleracea"

/mol_type="genomic DNA"

/strain="TO1000DH3"

/db_xref="taxon:3712"

/clone="BOHKT9"

/clone_lib="BOHK"

/note="Vector: PHOS1; Site 1: BstXI; 2-3 kb sheared genomic DNA inserted into PHOS1 using BstXI linkers"

ORIGIN

Query Match 68.9%; Score 91.6; DB 9; Length 763;

Best Local Similarity 81.5%; Pred. No. 6.7e-19;

Matches 106; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 4 CCCCCCGCGTTCATGATGATGATAGAGGCTGTGGATTGACGTAGGGGGCAG 63

DB 727 CCTTCGCTGATCGAATGATGATAGAGGCTGTGGATTGACGTAGGGGGCTAG 668

QY 64 GATGAGTATATTCTGGAGAGCACTCCGGCGAATAGCAAGCGCTTGATACAGTTGTA 123

DB 667 GGATGATATATTCTGGAGAGCACTCCAGCATATGAGCGCATGATACAGTTAT 608

QY 124 GGGAGGAGATT 133

DB 607 GACTTGGAAAT 598

RESULT 7

CG026604/c 764 bp DNA linear GSS 19-AUG-2003

LOCUS CG026604

DEFINITION PGAE30TF PGAA Carica papaya genomic clone PGAE30, genomic survey sequence.
 ACCESSION CG026604
 VERSION CG026604.1 GI:33898760
 KEYWORDS GSS.
 SOURCE Carica papaya (papaya)
 ORGANISM Carica papaya
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Caricaceae; Carica.
 1 (bases 1 to 764)
 Town, C.D., Van Aken, S., Utterback, T. and Fraese, C.M.
 TITLE Whole genome shotgun sequencing of Carica papaya
 JOURNAL Unpublished (2003)
 COMMENT Other GSSs: PGAE30TR
 CONTACT: Chris Town
 TIGR 9712 Medical Center Drive, Rockville, MD 20850, USA.
 Tel: 301-838-3523
 Fax: 301-838-0208
 Email: cdtown@tigr.org
 DNA provided by Ray Ming was isolated from cultivar Sundp that was transgenic for papaya ringspot virus coat protein gene
 Seq primer: TF
 Class: sheared ends.

FEATURES
 source
 1..764
 /organism="Carica papaya"
 /mol_type="genomic DNA"
 /cultivar="Sundp"
 /db_xref="taxon:3649"
 /clone="PGAE30"
 /note="Vector: pHOS1, Site 1: BstXI; 2-3 kb sheared genomic DNA inserted into pHOS1 using BstXI linkers"

ORIGIN
 Query Match 68.9%; Score 91.6; DB 10; Length 764;
 Best Local Similarity 85.1%; Pred. No. 6,7e-19;
 Matches 114; Conservative 0; Mismatches 19; Indels 1; Gaps 1;

QY 1 GCTCCCCCGCGTTCATGATGATGAAGAGGCTCGTGGATTGACGTAGGAGG 60
 662 GCTCCCCCGCGTTCATGATGATGAAGAGGCTCGTGGATTGACGTAGGAGG 603

DB 61 CAGGATGCGCTAAT-TTCTGGAGCGAATCCCGGCGCAATACGAAGCGCTTGATACAGT 119
 602 TAGGGATGCGCTAATTTCTGGAGCGAATCCCGGCGCAATATGAAGCGCATGATACAG 543

QY 120 TGTAGGAGGAGATT 133
 542 TTATGCTTGGAA 529

DB 542 TTATGCTTGGAA 529

RESULT 8
 CK767400 610 bp mRNA linear EST 09-JUN-2005
 LOCUS pam01-9ms1-a06 Persea americana cDNA clone pam01-9ms1-a06 5',
 DEFINITION mRNA sequence.
 ACCESSION CK767400
 VERSION CK767400.1 GI:42721434
 KEYWORDS EST.
 SOURCE Persea americana (avocado)
 ORGANISM Persea americana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; magnoliids; Laurales; Lauraceae; Persea.
 1 (bases 1 to 610)
 dePamphilis, C., Carlson, J., Ma, H., Soltis, D., Soltis, P.,
 Oppenheimer, D., Frohlich, M., Doyle, J., Tanksley, S., Webb, M.,
 Leebens-Wack, J., Landherr, L., Ilut, D. and Wall, K.
 TITLE Whole genome shotgun sequencing of Persea americana
 JOURNAL Unpublished (2003)

COMMENT Contact: Claude dePamphilis or James Leebens-Wack
 Mueller Laboratory
 Penn State University
 208 Mueller Laboratory, Department of Biology, ATTN Rm212, Penn
 State University, University Park, PA 16802, USA
 Tel: 814 863 6413
 Fax: 814 865 9131
 Email: cwds@psu.edu or jh110@psu.edu
 The sequence provided is trimmed of vector and low quality regions.
 Full sequence and original trace file are available from the Plant
 Genome Network website (<http://psn.cornell.edu>)
 Plate: pam01-9ms1 row: a column: 06
 Seq primer: M33F.

FEATURES
 source
 1..610
 /organism="Persea americana"
 /mol_type="mRNA"
 /db_xref="PGN:pam01-9ms1-a06"
 /db_xref="taxon:3435"
 /clone="pam01-9ms1-a06"
 /tissue_type="flower buds"
 /dev_stage="12-20 mm buds"
 /lab_host="SOLR"
 /clone_1ib="Pam01"
 /note="Vector: pBluescript SK (+/-); site_1: EcoRI; site_2: XhoI; This is a directionally cloned, non-normalized library. This library has been generated by the Floral Genome Project (FGP). The Floral Genome Project is funded by NSF's Plant Genome Research Program (DBI-0115684). More information about the project can be obtained at <http://fgp.bio.psu.edu>"

ORIGIN
 Query Match 68.6%; Score 91.2; DB 7; Length 610;
 Best Local Similarity 85.6%; Pred. No. 8.7e-19;
 Matches 113; Conservative 0; Mismatches 18; Indels 1; Gaps 1;

QY 1 GCTCCCCCGCGTTCATGATGATGAAGAGGCTCGTGGATTGACGTAGGAGG 60
 48 GCTCCCCCGCGTTCATGATGATGAAGAGGCTCGTGGATTGACGTAGGAGG 107

DB 61 CAGGATGCGCTAAT-TTCTGGAGCGAATCCCGGCGCAATACGAAGCGCTTGATACAGT 119
 108 TAGGGATGCGCTAATTTCTGGAGCGAATCCCGGCGCAATATGAAGCGCATGATACAG 167

QY 120 TGTAGGAGGAG 131
 168 CTTGGAATGAA 179

DB 168 CTTGGAATGAA 179

RESULT 9
 BH674012 839 bp DNA linear GSS 19-FEB-2002
 LOCUS BOMHD96TR_BO_2.3 KB Brassica oleracea genomic clone BOMHD96,
 DEFINITION genomic survey sequence.
 ACCESSION BH674012
 VERSION BH674012.1 GI:18742175
 KEYWORDS GSS.
 SOURCE Brassica oleracea
 ORGANISM Brassica oleracea
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
 1 (bases 1 to 839)
 Ayale, M., Haas, B.J., Kumar, N., Wu, H., Xiao, Y., Van Aken, S.,
 Utterback, T.R., Wortman, J.R., White, O.R. and Town, C.D.
 TITLE Whole genome shotgun sequencing of Brassica oleracea and its application to gene discovery and annotation in Arabidopsis
 JOURNAL Genome Res. 15 (4), 487-495 (2005)
 COMMENT PubMed 15805490
 CONTACT: Chris Town
 TIGR 9712 Medical Center Drive, Rockville, MD 20850, USA.


```
/note="Vector: pHOS1; Site_1: BstXI; 1.6-2 kb sheared
```

Search completed: April 18, 2006, 01:01:36
Job time : 2983 secs

11115 rage Blank (uspto)

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: April 17, 2006, 23:31:51 ; Search time 485 Seconds
(without alignments)
1827.637 Million cell updates/sec

Title: US-10-663-241-32

Perfect score: 133
Sequence: 1 gctcccccgcgcgtcgttca.....tacagtcgaggagggact 133

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_21.*
1: geneseqn1980s:*
2: geneseqn1980s:*
3: geneseqn2000s:*
4: geneseqn2000s:*
5: geneseqn2000s:*
6: geneseqn2000s:*
7: geneseqn2000s:*
8: geneseqn2000s:*
9: geneseqn2000s:*
10: geneseqn2000s:*
11: geneseqn2000s:*
12: geneseqn2000s:*
13: geneseqn2000s:*
14: geneseqn2000s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	133	100.0	133	2	AAV99599 Prm PEP
2	122	91.7	165	2	AAx21409 Prm Prom
3	122	91.7	168	2	AAx21407 Prm/rbcl
4	122	91.7	176	12	Adm01282 Plastid 1
5	122	91.7	1134	2	AAx21415 Plastid t
6	122	91.7	1134	2	AAx21415 Selectabl
7	122	91.7	1143	10	AdE06202 Nicotiana
8	122	91.7	1148	12	AdO85784 Chimeric
9	122	91.7	1332	12	AdO85782 Chimeric
10	122	91.7	1416	2	AAx21432 Regulator
11	122	91.7	1417	2	AAx21432 Regulator
12	122	91.7	1417	10	AdE06203 Plastid t
13	122	91.7	5834	12	AdM01283 Plastid P
14	122	91.7	6465	12	AdM01293 Plastid P
15	122	91.7	6659	12	AdM01290 Plastid P
16	122	91.7	7549	12	AdM01292 Plastid P
17	121	91.0	161	2	AAx21423 5' and 3'
18	121	91.0	1183	3	AAx21376 Nucleotid
19	121	91.0	1208	2	AAx21433 Regulator

20	121	91.0	1613	12	AdO85788 Chimeric
21	121	91.0	1920	13	AdR70709 DNA const
22	121	91.0	2145	8	Abx13738 Edited St
23	121	91.0	4671	3	AAx21385 Nucleotid
24	119.4	89.8	1544	8	Abx13719 pSAC114 v
25	119.4	89.8	2391	8	Abx13737 Scptomy
26	118.8	89.3	150	2	AAx21406 Prm/psba
27	117.8	88.6	4591	6	AbS5360 DNA seque
28	114.8	86.3	142	6	AbS5361 Nicotiana
29	107	80.5	119	14	AdX17034 Tobacco 1
30	102.8	77.3	184	4	AAx21408 targetin
31	102.8	77.3	201	2	AAx21408 targetin
32	102.8	77.3	220	6	AbS54934 DNA seque
33	102.8	77.3	233	13	AdT78239 Tobacco p
34	102.8	77.3	2569	12	AdI05018 apha-6/np
35	102.8	77.3	2962	2	AAx21408 targetin
36	102.8	77.3	3204	12	AdI05016 aada/BADH
37	102.8	77.3	3300	12	AdI05017 gfp/BADH
38	102.8	77.3	4363	9	ACC85346 PCB42-94
39	102.8	77.3	4363	10	AdE34324 Plastid t
40	102.8	77.3	4363	12	AdE34324 Plastid t
41	102.8	77.3	4746	10	AdE34240 Plastid P
42	102.8	77.3	6477	5	AAx16797 Chloropla
43	102.8	77.3	7652	12	AdO07359 Plastid t
44	102.8	77.3	8684	12	AdO07360 Plastid t
45	102.8	77.3	10011	12	AdO07377 Plastid t

ALIGNMENTS

RESULT 1	AAV99599	standard; DNA; 133 BP.
ID	AAV99599	
XX	AAV99599;	
AC	27-AUG-2003 (revised)	
DT	29-MAR-1999 (first entry)	
XX	Prm PEP promoter.	
DE	Promoter; nuclear encoded plastid RNA polymerase; NEP;	
XX	KW Plastid encoded plastid RNA polymerase; PEP; Prm; chloroplast;	
KW	transgenic plant; maize; ss.	
XX	Unidentified.	
OS	Unidentified.	
XX	Unidentified.	
PN	WO9855595-A1.	
XX	10-DEC-1998.	
PD	03-JUN-1998; 98WO-US011437.	
XX	03-JUN-1997; 97US-0048376P.	
PR	12-SEP-1997; 97US-0058670P.	
XX	(RUTF) UNIV RUTGERS STATE NEW JERSEY.	
PA	Malgia P, Silhavy D, Sritaman P;	
PI	WPI; 1999-070262/06.	
DR	Isolated nuclear-encoded plastid RNA polymerase promoter sequences -	
PT	useful for expressing exogenous protein in plant plastids such as	
PT	chloroplasts.	
XX	Disclosure; Page 4; 79p; English.	
PS	This is the nucleotide sequence of plasmid-encoded plastid RNA polymerase	
CC	(PEP) Prm promoter. Isolated rpb, acp, ctp and 16S rDNA promoter	
CC	elements (see AAV99599-99) or homologues are used for producing exogenous	
CC	proteins of interest in plant plastids. Also new is a DNA construct for	

CC stably transforming the plasmids of higher plants comprising: (i) a
CC transcription unit encoding at least one exogenous protein of interest,
CC and (ii) a first nuclear-encoded plastid (NEP) RNA polymerase promoter,
CC and a second NEP RNA polymerase promoter in tandem operably linked to the
CC transcription unit, where expression of the transcription unit is
CC regulated by the promoters. Use of the novel constructs facilitates
CC transformation of a wide range of plant species, allowing ubiquitous
CC expression of a transforming DNA in plastids (e.g. chloroplasts) of
CC multicellular plants. Preferred promoter combinations are the Prrn NEP
CC promoters combined with clp type II NEP promoter in dicots and the Prrn
CC NEP promoter combined with the clp type II NEP promoter in monocots and
CC dicots. (Updated on 27-AUG-2003 to correct OS field.)

XX Sequence 133 BP; 30 A; 25 C; 50 G; 28 T; 0 U; 0 Other;

Query Match 100.0%; Score 133; DB 2; Length 133;

Best Local Similarity 100.0%; Pred. No. 3.2e-37; Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCCCGCCGCTGTTCAATGAGATGATGATGAGGCTGTTGATTCAGCTGAGGGG 60
DB 1 GCTCCCGCCGCTGTTCAATGAGATGATGATGAGGCTGTTGATTCAGCTGAGGGG 60

QY 61 CAGGATGGCTATATTCTTGGGAGCGAATCTCCGGCGAATGCAAGCGCTTGATACAGTT 120
DB 61 CAGGATGGCTATATTCTTGGGAGCGAATCTCCGGCGAATGCAAGCGCTTGATACAGTT 120

QY 121 GTAGGGAGGAGATT 133
DB 121 GTAGGGAGGAGATT 133

RESULT 2

AAAX21409

ID AAAX21409 standard; DNA; 165 BP.

XX AAAX21409;

XX 21-MAY-1999 (first entry)

XX Prrn promoter sequence.

XX Construct; marker; antibiotic resistance; regulatory sequence; promoter;
XX stabilizing sequence; plastid; plant; ss.

XX Synthetic.

XX Nicotiana tabacum.

XX US5877402-A.

XX 02-MAR-1999.

XX 31-JAN-1994; 94US-00189256.

XX 01-MAY-1990; 90US-00518763.

XX 25-AUG-1993; 93US-00111398.

XX (RUTP) UNIV RUTGERS STATE NEW JERSEY.

XX Maliqa ZS, Maliqa P, Staub JM;

XX WPI; 1999-189744/16.

XX New DNA construct containing an antibiotic resistance marker - useful for
XX stably transforming the plastids of multicellular plants.

XX Disclosure; Fig 18A; 101pp; English.

XX The invention relates to a DNA construct, containing a non-lethal stable
XX marker (e.g. antibiotic resistance) under the control of a 5' regulatory
XX sequence and a 3' stabilizing sequence, for stably transforming the
XX plastids of multicellular plants and allowing expression of heterologous
XX proteins especially non-native plastid or plant proteins. This sequence

CC corresponds to the 16S ribosomal RNA operon promoter (Prrn)
XX Sequence 165 BP; 40 A; 31 C; 61 G; 33 T; 0 U; 0 Other;

Query Match 91.7%; Score 122; DB 2; Length 165;
Best Local Similarity 99.3%; Pred. No. 2.9e-33;
Matches 133; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 GTCCTCCCGCCGCTGTTCAATGAGATGATGATGAGGCTGTTGATTCAGCTGAGGGG 60
DB 1 GTCCTCCCGCCGCTGTTCAATGAGATGATGATGAGGCTGTTGATTCAGCTGAGGGG 60

QY 61 CAGGATGGCTATATTCTTGGGAGCGAATCTCCGGCGAATGCAAGCGCTTGATACAGT 119
DB 61 CAGGATGGCTATATTCTTGGGAGCGAATCTCCGGCGAATGCAAGCGCTTGATACAGT 120

QY 120 TGTAGGGAGGAGATT 133
DB 121 TGTAGGGAGGAGATT 134

RESULT 3

AAAX21407

ID AAAX21407 standard; DNA; 168 BP.

XX AAAX21407;

XX 21-MAY-1999 (first entry)

XX Prrn/rbcl/Rubisco regulatory region.

XX Construct; marker; antibiotic resistance; regulatory sequence; promoter;
XX stabilizing sequence; plastid; plant; ss.

XX Synthetic.

XX Nicotiana tabacum.

XX US5877402-A.

XX 02-MAR-1999.

XX 31-JAN-1994; 94US-00189256.

XX 01-MAY-1990; 90US-00518763.

XX 25-AUG-1993; 93US-00111398.

XX (RUTP) UNIV RUTGERS STATE NEW JERSEY.

XX Maliqa ZS, Maliqa P, Staub JM;

XX WPI; 1999-189744/16.

XX New DNA construct containing an antibiotic resistance marker - useful for
XX stably transforming the plastids of multicellular plants.

XX Disclosure; Fig 8; 101pp; English.

XX The invention relates to a DNA construct, containing a non-lethal stable
XX marker (e.g. antibiotic resistance) under the control of a 5' regulatory
XX sequence and a 3' stabilizing sequence, for stably transforming the
XX plastids of multicellular plants and allowing expression of heterologous
XX proteins especially non-native plastid or plant proteins. This sequence
XX corresponds to the regulatory region of the plasmid pTNH32 and comprises
XX the 16S ribosomal RNA operon promoter (Prrn), the rbcl leader sequence
XX including the ribosome binding site and the first 5 amino acids coding
XX sequence from the ribulose-1,5-bisphosphate decarboxylase/oxygenase large
XX subunit (Rubisco) gene

XX Sequence 168 BP; 44 A; 32 C; 57 G; 35 T; 0 U; 0 Other;

Query Match 91.7%; Score 122; DB 2; Length 168;

Best Local Similarity 99.3%; Pred. No. 2.9e-33; Matches 133; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 GCTCCCCCGCGTCGTTCAATGAGATGATTAAGAGCGTCGTGGATTGACGTAGAGGGG 60
Db 1 GCTCCCCCGCGTCGTTCAATGAGATGATTAAGAGCGTCGTGGATTGACGTAGAGGGG 60
QY 61 CAGGATGCGCTATA-TTCTGGAGAGCGAATCTCCGGCGAATACGAAGCGCTTGATACAGT 119
Db 61 CAGGATGCGCTATA-TTCTGGAGAGCGAATCTCCGGCGAATACGAAGCGCTTGATACAGT 120
QY 120 TGTAGGAGGAGGATT 133
Db 121 TGTAGGAGGAGGATT 134

RESULT 4
ADM01282
ID ADM01282 standard; DNA; 176 BP.
AC ADM01282;
XX
XX
XX 01-JUL-2004 (first entry)
XX
XX
XX Plasmid 16S ribosomal RNA subunit promoter sequence.
DE
XX vector; plasmid; artificial intergene region; plant;
XX transplastomic angiosperm; agronomic property; stress resistance;
KM rbcL gene; ds.
XX
XX Unidentified.
OS
XX WO2004029256-A2.
PN
XX 08-APR-2004.
PD
XX 15-SEP-2003; 2003WO-CU000009.
PF
XX 27-SEP-2002; 2002CU-00000208.
PR
XX (INGG-) CENT ING GENETICA & BIOTECNOLOGIA.
PA
XX Selman-Housein Sosa G, Aguilar Cabeza E, Gonzalez Quintero ADC;
PI Ramos Gonzalez O;
XX
XX WPI; 2004-316131/29.
DR
XX
XX DNA vector for transformation and expression in plasmids, useful e.g. for
PT producing pharmaceutical proteins or improving agronomic properties, has
PT gene inserted in artificial intergene region.
XX
XX
XX Example 1; SEQ ID NO 14; 74pp; Spanish.
PS
XX The invention relates to a DNA vector (A) for stable transformation and
CC expression of genes (I) in plasmids, where (I) is inserted in an
CC artificial intergene region (AIR) formed by combining two 5'-untranslated
CC regions (5'-UTRs) of genes that transcribe in different directions and
CC are derived from plants of different divisions or classes. (A) are used
CC to produce transplastomic angiosperms that have improved agronomic
CC properties (e.g. resistance to biotic or abiotic stress) or express a
CC very wide range of agricultural, veterinary, pharmaceutical, nutritional
CC or industrial products, e.g. enzymes, vaccinating antigens, cytokines or
CC immunoglobulins. Use of (A) eliminates the need for a transposon for gene
CC insertion; inserted genes do not require promoters and terminators; and
CC the structure of flanking sequences in (A) ensures universal
CC applicability. Also any selection marker in (A) can be eliminated by
CC homologous recombination. (A) provides efficient and stable expression of
CC genes without causing any functional alterations. This sequence
CC represents the plasmid 16S ribosomal RNA subunit promoter sequence used
CC to generate the vectors of the invention.
CC
XX Sequence 176 BP; 39 A; 37 C; 60 G; 40 T; 0 U; 0 Other;
SQ

Query Match 91.7%; Score 122; DB 12; Length 176;
Best Local Similarity 99.3%; Freq. No. 2.9e-33;

Matches 133; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1 GCTCCCCCGCGTCGTTCAATGAGATGATTAAGAGCGTCGTGGATTGACGTAGAGGGG 60
Db 16 GCTCCCCCGCGTCGTTCAATGAGATGATTAAGAGCGTCGTGGATTGACGTAGAGGGG 75
QY 61 CAGGATGCGCTATA-TTCTGGAGAGCGAATCTCCGGCGAATACGAAGCGCTTGATACAGT 119
Db 76 CAGGATGCGCTATA-TTCTGGAGAGCGAATCTCCGGCGAATACGAAGCGCTTGATACAGT 135
QY 120 TGTAGGAGGAGGATT 133
Db 136 TGTAGGAGGAGGATT 149

RESULT 5
AAT85195/c
ID AAT85195 standard; DNA; 1134 BP.
AC AAT85195;
XX
XX
XX 10-MAR-1998 (first entry)
XX
XX
XX Plasmid targeting region of plasmid pGS31A.
DE
XX
XX Plasmid; transformation; transplastomic plant; transgenic plant;
XX Brassica; cruciferous plant; vector; plasmid pGS31A.
KM spectinomycin resistance; selectable marker; aadA gene; ss.
XX
XX Arabidopsis thaliana.
OS
XX Synthetic.
OS
XX Chimeric.
OS
XX WO9732977-A1.
PN
XX 12-SEP-1997.
PD
XX 06-MAR-1997; 97WO-US003444.
PF
XX 06-MAR-1996; 96US-0012916P.
PR
XX (RUTF) UNIV RUTGERS STATE NEW JERSEY.
PA
XX Maliga P, Sikdar SR, Reddy SV;
PI
XX WPI; 1997-470543/43.
DR
XX
XX Production of transplastomic plants - by transfection with plasmid
PT targeted DNA, specifically for Cruciferous plants.
PT
XX
XX Disclosure; Fig 6; 45pp; English.
PS
XX This sequence comprises the plasmid targeting region of plasmid pGS31A.
CC This plasmid carries a spectinomycin resistance gene (aadA) flanked by
CC Arabidopsis plasmid DNA sequences that target its insertion between trnV
CC and the rps 12/7 operon. It was produced by ligating the chimeric aadA
CC gene from Ec11236II into the unique HincII site of plasmid pGS7 (see
CC AAT85194). A novel method of production of transplastomic plants
CC involves: delivering transforming DNA, preferably cloned in pGS31A,
CC pGS85A or pGS7, to a plasmid genome of plant cells in culture, selecting
CC cells with transformed plasmids and regenerating these to plants. The
CC transforming DNA comprises (i) (i) several targeting sequences (i.e.
CC plasmid DNA sequences from the genome to be transformed) to allow
CC homologous recombination, (ii) 5' and 3' regulatory regions from plasmid
CC DNA linked to an antibiotic resistance gene for use as selection marker,
CC (iii) similar regulatory regions controlling a foreign gene of interest,
CC and (iv) at least one cloning site for insertion of the foreign gene
CC adjacent to the marker gene. The method is used to transform cruciferous
CC plants, e.g. Brassica species. The combination of homologous
CC recombination, selectable marker and use of plasmid regulatory sequences
CC improves generation of stably transformed plants. Expression of foreign
CC genes in plasmids, rather than in the nucleus, avoids risk of
CC transmitting the foreign gene in the pollen, provides high levels of

CC protein expression, permits simultaneous incorporation of several genes
CC and avoids the positional effects and gene silencing associated with
CC nuclear transformation

XX Sequence 1134 BP; 295 A; 310 C; 248 G; 281 T; 0 U; 0 Other;

Query Match 91.7%; Score 122; DB 2; Length 1134;
Best Local Similarity 99.3%; Pred. No. 5.2e-33;
Matches 133; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 GGTCCCCCGCGCTTCATATGAGATGATTAAGAGCTCTGGGATTGACGTGAGGGG 60

DB 1130 GGTCCCCCGCGCTTCATATGAGATGATTAAGAGCTCTGGGATTGACGTGAGGGG 1071

QY 61 CAGGATGGCTATA-TTCTGGAGCGAATCTCGGGCGAATACGAAGCGCTTGATACACT 119

DB 1070 CAGGATGGCTATATTTCTGGAGCGAATCTCGGGCGAATACGAAGCGCTTGATACACT 1011

QY 120 TGTAGGAGGAGATT 133

DB 1010 TGTAGGAGGAGATT 997

RESULT 6
AAx21415/c
ID AAx21415 standard; DNA; 1134 BP.

AC AAx21415;

DT 21-MAY-1999 (first entry)

DE Selectable marker gene for plasmid pPRV112A.

KW Construct; marker; antibiotic resistance; regulatory sequence; promoter;
KW stabilizing sequence; plastid; plant; ss.

OS Synthetic.

PN US5877402-A.

PD 02-MAR-1999.

PF 31-JAN-1994; 94US-00189256.

PR 01-MAY-1990; 90US-00518763.

PR 25-AUG-1993; 93US-00111398.

PA (RUTF) UNIV RUTGERS STATE NEW JERSEY.

PI Maliga ZS, Maliga P, Staub JM;

DR WPI, 1999-189744/16.

PT New DNA construct containing an antibiotic resistance marker - useful for
PT stably transforming the plastids of multicellular plants.

PS Claim 21; Fig 20E; 101bp; English.

CC The invention relates to a DNA construct, containing a non-lethal stable
CC marker (e.g. antibiotic resistance) under the control of a 5' regulatory
CC sequence and a 3' stabilizing sequence, for stably transforming the
CC plastids of multicellular plants and allowing expression of heterologous
CC proteins especially non-native plastid or plant proteins. This sequence
CC corresponds to the selectable marker gene for the plasmid pPRV112A

XX Sequence 1134 BP; 291 A; 303 C; 257 G; 283 T; 0 U; 0 Other;

Query Match 91.7%; Score 122; DB 2; Length 1134;
Best Local Similarity 99.3%; Pred. No. 5.2e-33;
Matches 133; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 GGTCCCCCGCGCTTCATATGAGATGATTAAGAGCTCTGGGATTGACGTGAGGGG 60

DB 1058 GGTCCCCCGCGCTTCATATGAGATGATTAAGAGCTCTGGGATTGACGTGAGGGG 999

QY 61 CAGGATGGCTATA-TTCTGGAGCGAATCTCGGGCGAATACGAAGCGCTTGATACACT 119

DB 998 CAGGATGGCTATATTTCTGGAGCGAATCTCGGGCGAATACGAAGCGCTTGATACACT 939

QY 120 TGTAGGAGGAGATT 133

DB 938 TGTAGGAGGAGATT 925

RESULT 7
ADE06202/c
ID ADE06202 standard; DNA; 1143 BP.

AC ADE06202;

DT 29-JAN-2004 (first entry)

DE Nicotiana tabacum targeting region of plasmid pGS31A.

KW Vector; pZS391B; plastid transformation; higher plant; transgene;
KW Brassica plant; transplastomic plant; DNA delivery; targeting region;
KW plasmid pGS31A; plant; ds.

OS Nicotiana tabacum.

PN US2003200568-A1.

PD 23-OCT-2003.

PF 12-JUN-2003; 2003US-00460716.

PR 06-MAR-1997; 97MO-US003444.

PR 05-FEB-1999; 98US-00142114.

PR 13-MAR-2000; 2000US-00524087.

XX (MALI/) MALIGA P.

PA (SKAR/) SKARJINSKAIA M.

PA (MALI/) MALIGA Z S.

PI Maliga P, Skarjinskaia M, Maliga ZS;

DR WPI, 2003-852834/79.

PT New improved vector for transforming plastids of higher plants and
PT comprising a targeting segment having first and second chimeric targeting
PT sequences, useful for creating transplastomic plants.
PS Disclosure; SEQ ID NO 2; 35bp; English.

CC The present invention relates to a new improved vector (pZS391B) for
CC transforming plastids of higher plants. The vector comprises a targeting
CC segment having first and second chimeric targeting sequences for
CC facilitating recombination within the plastid genome, each of which
CC flanks at least one transgene of interest and has a first portion derived
CC from the plant species being targeted for transformation, and a second
CC portion derived from a different plant species. The transgene constitutes
CC a monocistronic or polycistronic expression unit comprising a selectable
CC marker gene and a foreign gene of interest. It encodes a selectable
CC marker, herbicide resistance or drought resistance gene. The selectable
CC marker gene comprises kanamycin, streptomycin or spectinomycin. The
CC plastids are chloroplasts. The vector is useful for transforming plastids
CC of higher plants (e.g. Brassica plants), and for creating transplastomic
CC plants. The methods and compositions of the invention facilitate the
CC regeneration of transformed plants following the delivery of beneficial
CC DNA molecules. The present sequence represents Nicotiana tabacum
CC targeting region of plasmid pGS31A.

XX Sequence 1143 BP; 297 A; 313 C; 252 G; 281 T; 0 U; 0 Other;

Query Match 91.7%; Score 122; DB 10; Length 1143;
Best Local Similarity 99.3%; Pred. No. 5.2e-33;

Matches 133; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

```
QY 1 GCTCCCCCGCGTCTCAATGAGATGATTAAGAGCGCTGTGGATTGACGTAGGGGG 60
DB 1130 GCTCCCCCGCGTCTCAATGAGATGATTAAGAGCGCTGTGGATTGACGTAGGGGG 1071
QY 61 CAGGGATGGCTATATTTCTGGAGCGAATCTCCGGCGAATACGAAGCGCTTGATACAGT 119
DB 1070 CAGGGATGGCTATATTTCTGGAGCGAATCTCCGGCGAATACGAAGCGCTTGATACAGT 1011
QY 120 TGTAGGAGGAGGATT 133
DB 1010 TGTAGGAGGAGGATT 997
```

RESULT 8

AD085784 standard; DNA; 1148 BP.

```
XX AC AD085784;
XX DT 09-SEP-2004 (first entry)
XX DE Chimeric gene AADA-129 SEQ ID NO:3.
XX KM ds; gene; elementary chimeric gene; hydroxyphenyl pyruvate dioxigenase;
XX KM HPPD; plant; weed control; herbicide.
XX OS Nicotiana tabacum.
XX OS Chimeric.
```

```
XX FH Key Location/Qualifiers
XX FT CDS 136..930
XX FT /*tag= a
XX FT /product= "AADA-129"
```

FR2848568-A1.

18-JUN-2004.

17-DEC-2002; 2002FR-00015975.

17-DEC-2002; 2002FR-00015975.

(RHOB-) RHOBIO SA.

Tisot G, Wisniewski JP, Ferullo JM;

WPI; 2004-452915/43.

P-PSDB; AD085785.

PT New chimeric gene including a sequence for hydroxyphenyl pyruvate
dioxigenase, useful for preparing transgenic plants resistant to
herbicides that target this enzyme, by plastid transformation.

Example 1; SEQ ID NO 3; 47pp; French.

XX The invention relates to a novel chimeric gene (CG) comprising at least
XX one elementary chimeric gene (ecG) that consists of, functionally linked
XX in the direction of transcription, a promoter (P), functional in plants,
XX a sequence encoding hydroxyphenyl pyruvate dioxigenase (HPPD) and a
XX terminator, functional in plants. The chimeric genes of the invention are
XX used to impart resistance to herbicides that target HPPD, so that plants
XX containing CG can be safely treated, for weed control, with these
XX herbicides. Plastid transformation, which involves a double homologous
XX recombination, is precisely targeted, avoiding positional effects that
XX occur during nuclear transgenesis. The present sequence represents an
XX elementary chimeric gene of the invention.

SQ Sequence 1148 BP; 314 A; 256 C; 307 G; 271 T; 0 U; 0 Other;

Query Match 91.7%; Score 122; DB 12; Length 1148;
Best Local Similarity 99.3%; Pred. No. 5; 2e-33;

Matches 133; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

```
QY 1 GCTCCCCCGCGTCTCAATGAGATGATTAAGAGCGCTGTGGATTGACGTAGGGGG 60
DB 1 GCTCCCCCGCGTCTCAATGAGATGATTAAGAGCGCTGTGGATTGACGTAGGGGG 60
QY 61 CAGGGATGGCTATATTTCTGGAGCGAATCTCCGGCGAATACGAAGCGCTTGATACAGT 119
DB 61 CAGGGATGGCTATATTTCTGGAGCGAATCTCCGGCGAATACGAAGCGCTTGATACAGT 120
QY 120 TGTAGGAGGAGGATT 133
DB 121 TGTAGGAGGAGGATT 134
```

RESULT 9

AD085782 standard; DNA; 1332 BP.

```
XX AC AD085782;
XX DT 09-SEP-2004 (first entry)
XX DE Chimeric gene AADA-111 SEQ ID NO:1.
XX KM ds; gene; elementary chimeric gene; hydroxyphenyl pyruvate dioxigenase;
XX KM HPPD; plant; weed control; herbicide.
XX OS Nicotiana tabacum.
XX OS Chimeric.
```

```
XX FH Key Location/Qualifiers
XX FT CDS 136..930
XX FT /*tag= a
XX FT /product= "AADA-111"
```

FR2848568-A1.

18-JUN-2004.

17-DEC-2002; 2002FR-00015975.

17-DEC-2002; 2002FR-00015975.

(RHOB-) RHOBIO SA.

Tisot G, Wisniewski JP, Ferullo JM;

WPI; 2004-452915/43.

P-PSDB; AD085783.

PT New chimeric gene including a sequence for hydroxyphenyl pyruvate
dioxigenase, useful for preparing transgenic plants resistant to
herbicides that target this enzyme, by plastid transformation.

Example 1; SEQ ID NO 1; 47pp; French.

XX The invention relates to a novel chimeric gene (CG) comprising at least
XX one elementary chimeric gene (ecG) that consists of, functionally linked
XX in the direction of transcription, a promoter (P), functional in plants,
XX a sequence encoding hydroxyphenyl pyruvate dioxigenase (HPPD) and a
XX terminator, functional in plants. The chimeric genes of the invention are
XX used to impart resistance to herbicides that target HPPD, so that plants
XX containing CG can be safely treated, for weed control, with these
XX herbicides. Plastid transformation, which involves a double homologous
XX recombination, is precisely targeted, avoiding positional effects that
XX occur during nuclear transgenesis. The present sequence represents an
XX elementary chimeric gene of the invention.

SQ Sequence 1332 BP; 341 A; 272 C; 329 G; 390 T; 0 U; 0 Other;

Query Match 91.7%; Score 122; DB 12; Length 1332;
Best Local Similarity 99.3%; Pred. No. 5; 4e-33;

Matches 133; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 GGTCCCCCGCGTTCATGATGATGATAGAGGCTCGTGGGATTGACGTTGAGGGGG 60
 |||
 Db 1 GGTCCCCCGCGTTCATGATGATGATAGAGGCTCGTGGGATTGACGTTGAGGGGG 60
 |||

QY 61 CAGGATGCGCTATA-TTCTGGAGCGAACTCCGGCGGAATACGAACGCTTGATACAGT 119
 |||
 Db 61 CAGGATGCGCTATA-TTCTGGAGCGAACTCCGGCGGAATACGAACGCTTGATACAGT 120
 |||

QY 120 TGTAGGAGGAGATT 133
 |||
 Db 121 TGTAGGAGGAGATT 134
 |||

RESULT 10
 AAX21432
 ID AAX21432 standard; DNA; 1416 BP.

AC AAX21432;
 XX
 XX
 DT 21-MAY-1999 (first entry)
 XX
 DE Regulatory region Prrn(L)/Rbcl(S)/kan/TpsbA(L).
 XX
 KW Construct; marker; antibiotic resistance; regulatory sequence; promoter;
 XX stabilizing sequence; plasmid; plant; ss.
 XX
 OS Synthetic.
 XX
 PN US877402-A.
 XX
 PD 02-MAR-1999.
 XX
 PF 31-JAN-1994; 94US-00189256.
 XX
 PR 01-MAY-1990; 90US-00518763.
 XX
 PR 25-AUG-1993; 93US-00111398.
 XX
 XX
 PA (RUTP) UNIV RUTGERS STATE NEW JERSEY.
 XX
 PI Maliga ZS, Maliga P, Straub JM;
 XX
 DR WPI; 1999-189744/16.
 XX
 PT New DNA construct containing an antibiotic resistance marker - useful for
 XX stably transforming the plasmids of multicellular plants.
 XX
 PS Disclosure; Fig 28A; 101pp; English.
 XX
 CC The invention relates to a DNA construct, containing a non-lethal stable
 CC marker (e.g. antibiotic resistance) under the control of a 5' regulatory
 CC sequence and a 3' stabilizing sequence, for stably transforming the
 CC plasmids of multicellular plants and allowing expression of heterologous
 CC proteins especially non-native plasmid or plant proteins. This sequence
 CC corresponds to the regulatory region Prrn(L)/Rbcl(S)/kan/TpsbA(L) from
 CC the plasmid pTWH7
 CC
 SQ Sequence 1416 BP; 312 A; 322 C; 379 G; 403 T; 0 U; 0 Other;

Query Match 91.7%; Score 122; DB 2; Length 1416;
 Best Local Similarity 99.3%; Pred. No. 5.5e-33;
 Matches 133; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 GGTCCCCCGCGTTCATGATGATGATAGAGGCTCGTGGGATTGACGTTGAGGGGG 60
 |||
 Db 22 GGTCCCCCGCGTTCATGATGATGATAGAGGCTCGTGGGATTGACGTTGAGGGGG 81
 |||

QY 61 CAGGATGCGCTATA-TTCTGGAGCGAACTCCGGCGGAATACGAACGCTTGATACAGT 119
 |||
 Db 82 CAGGATGCGCTATA-TTCTGGAGCGAACTCCGGCGGAATACGAACGCTTGATACAGT 141
 |||

QY 120 TGTAGGAGGAGATT 133
 |||

Db 142 TGTAGGAGGAGATT 155
 |||

RESULT 11
 AAT85196
 ID AAT85196 standard; DNA; 1417 BP.
 XX
 AC AAT85196;
 XX
 DT 10-MAR-1998 (first entry)
 XX
 DE Plasmid targeting region of plasmid pGS85A.
 XX
 KW Plasmid; transformation; transplasmomic plant; transgenic plant;
 KW Brassica; cruciferous plant; vector; plasmid pGS85A;
 KW kanamycin resistance; neomycin phosphotransferase; neo gene;
 KW selectable marker; ss.
 XX
 XX Arabidopsis thaliana.
 OS Synthetic.
 OS Chimeric.
 XX
 FH Key Location/Qualifiers
 FT CDS 158..970
 FT /tag= a
 FT /note= "kanamycin resistance gene"
 XX
 PN WO9732977-A1.
 XX
 PD 12-SEP-1997.
 XX
 PF 06-MAR-1997; 97WO-US003444.
 XX
 PR 06-MAR-1996; 96US-0012916P.
 XX
 XX
 PA (RUTP) UNIV RUTGERS STATE NEW JERSEY.
 XX
 PI Maliga P, Sikdar SR, Reddy SV;
 XX
 DR WPI; 1997-470543/43.
 XX
 PT Production of transplasmomic plants - by transfection with plasmid
 XX targeted DNA, specifically for Cruciferous plants.
 XX
 PS Disclosure; Fig 7; 45pp; English.
 XX
 CC This sequence comprises the plasmid targeting region of plasmid pGS85A.
 CC This plasmid carries a neomycin phosphotransferase (neo) gene that
 CC confers kanamycin resistance gene, flanked on both sides by Arabidopsis
 CC plasmid targeting sequences. It was produced by ligating the neo gene
 CC into the unique HincII site of plasmid pGS7 (see AAT85194). A novel
 CC method of producing transplasmomic plants involves delivering
 CC transforming DNA, preferably cloned in pGS31A, pGS85A or pGS7, to a
 CC plasmid genome of plant cells in culture, selecting cells with
 CC transformed plasmids and regenerating these to plants. Transforming DNA
 CC comprises (i) (i) several targeting sequences (i.e. plasmid DNA
 CC sequences from the genome to be transformed) to allow homologous
 CC recombination. (ii) 5' and 3' regulatory regions from plasmid DNA linked
 CC to a selectable marker gene, (iii) regulatory regions controlling a
 CC foreign gene of interest, and (iv) a cloning site for insertion of the
 CC foreign gene adjacent to the marker gene. The method is used to transform
 CC cruciferous plants, e.g. Brassica species. The combination of homologous
 CC recombination, selectable marker and use of plasmid regulatory sequences
 CC improves generation of stably transformed plants. Expression of foreign
 CC genes in plasmid, rather than in the nucleus, avoids risk of
 CC transmitting the foreign gene in the pollen, provides high levels of
 CC protein expression, permits simultaneous incorporation of several genes
 CC and avoids the positional effects and gene silencing associated with
 CC nuclear transformation
 CC
 SQ Sequence 1417 BP; 312 A; 323 C; 379 G; 403 T; 0 U; 0 Other;

Query Match	91.7%	Score 122	DB 2	Length 1417
Best Local Similarity	99.3%	Pred. No. 5	Se-33	
Matches 133	Conservative 0	Mismatches 0	Indels 1	Gaps 1
Qy	1	GGTCCCCCGCCGCTTCATAGAGATGATAAGAGCGCTGTGGGATTTGACGTGAGGGGG	60	
Db	23	GCTCCCCCGCCGCTTCATAGAGATGATAAGAGCGCTGTGGGATTTGACGTGAGGGGG	82	
Qy	61	CAGGAGTGGCTATA-TTCTGGAGACCACTCCGGGCAATACGAAGCGCTTGATACAGT	119	
Db	83	CAGGAGTGGCTATATTCTGGAGACCACTCCGGGCAATACGAAGCGCTTGATACAGT	142	
Qy	120	TGTAGGAGGAGGATT	133	
Db	143	TGTAGGAGGAGGATT	156	
RESULT 12				
ADE06203				
ID	ADE06203 standard, DNA; 1417 BP.			
XX	ADE06203;			
XX	AC			
XX	29-JAN-2004 (first entry)			
XX	Placitid targeting region of plasmid pGS85A.			
DE	Vector; pZS391B; plactid transformation; higher plant; transgene;			
KW	Brassica plant; transplasmic plant; DNA delivery; targeting region;			
KW	plasmid pGS85A; db.			
OS	Unidentified.			
XX	US2003200568-A1.			
PN	12-JUN-2003; 2003US-00460716.			
PF	06-MAR-1997; 97WMO-US003444.			
PR	05-FEB-1999; 99US-00142114.			
PR	13-MAR-2000; 2000US-00524087.			
PA	(MALI/) MALIGA P.			
PA	(SKAR/) SKARJINSKAIA M.			
PA	(MALI/) MALIGA Z S.			
PI	Maliga P, Skarjinskaia M, Maliga ZS;			
DR	WPI; 2003-852834/79.			
PT	New improved vector for transforming plactids of higher plants and			
PT	comprising a targeting segment having first and second chimeric targeting			
PT	sequences, useful for creating transplasmic plants.			
XX	Disclosure; SEQ ID NO 3; 35pp; English.			
XX	The present invention relates to a new improved vector (pZS391B) for			
XX	transforming plactids of higher plants. The vector comprises a targeting			
CC	segment having first and second chimeric targeting sequences for			
CC	facilitating recombination within the plactid genome, each of which			
CC	flanks at least one transgene of interest and has a first portion derived			
CC	from the plant species being targeted for transformation, and a second			
CC	portion derived from a different plant species. The transgene constitutes			
CC	a monocistronic or polycistronic expression unit comprising a selectable			
CC	marker gene and a foreign gene of interest. It encodes a selectable			
CC	marker, herbicide resistance or drought resistance gene. The selectable			
CC	marker gene comprises kanamycin, streptomycin or spectinomycin. The			
CC	plactids are chloroplasts. The vector is useful for transforming plactids			
CC	of higher plants (e.g. Brassica plants), and for creating transplasmic			
CC	plants. The methods and compositions of the invention facilitate the			
CC	regeneration of transformed plants following the delivery of beneficial			
CC	DNA molecules. The present sequence represents the plactid targeting			

CC	region of plasmid pGS85A.
XX	
SQ	Sequence 1417 BP; 312 A; 323 C; 379 G; 403 T; 0 U; 0 Other;
	Query Match 91.7%; Score 122; DB 10; Length 1417;
	Best Local Similarity 99.3%; Pred. No. 5.5e-33;
	Matches 133; Conservative 0; Mismatches 0; Indels 1; Gaps 1
OY	1 GCTCCCCCGCGTTCATGAGAAATGATTAAGAGCTCGTGGAATTGACGTGAGGGG 60
DB	23 GCTCCCCCGCGTTCATGAGAAATGATTAAGAGCTCGTGGAATTGACGTGAGGGG 82
OY	61 CAGGATGCGCTATA-TTCTGGAGGCACTCCGGCGAATACGAAGCCTTGATACAGT 119
DB	83 CAGGATGCGCTATATTCTCGGAGGCAACTCCGGCGAATACGAAGCCTTGATACAGT 142
OY	120 TGTAGGAGGGAATT 133
DB	143 TGTAGGAGGGAATT 156
RESULT 13	
ID	ADM01283 standard; DNA; 5834 BP.
XX	
AC	ADM01283;
XX	
DT	01-JUL-2004 (first entry)
XX	
DE	Plasmid pVTPA DNA sequence.
XX	
KX	vector; plasmid; artificial intergene region; plant;
KW	transplastomic angiosperm; agronomic property; stress resistance;
XX	rbdL gene; ds.
OS	Synthetic.
PN	MO2004029256-A2.
PB	08-APR-2004.
XX	
PF	15-SEP-2003; 2003MO-CUO00009.
PR	27-SEP-2002; 2002CU-00000208.
XX	
PA	(INGG-) CENT ING GENETICA & BIOTECNOLOGIA.
PI	Selman-Housein Sosa G, Aguilar Cabeza E, Gonzalez Quintero ADC,
PT	Ramos Gonzalez O;
DR	WP1; 2004-316131/29..
XX	
PS	Example 1; SEQ ID NO 15; 74pp; Spanish.
XX	
CC	The invention relates to a DNA vector (A) for stable transformation and
CC	expression of genes (I) in plastids, where (II) is inserted in an
CC	artificial intergene region (AIR) formed by combining two 5'-untranslated
CC	regions (5'-UTRs) of genes that transcribe in different directions and
CC	are derived from plants of different divisions or classes. (A) are used
CC	to produce transplastomic angiosperms that have improved agronomic
CC	properties (e.g. resistance to biotic or abiotic stress) or express a
CC	very wide range of agricultural, veterinary, pharmaceutical, nutritional
CC	or industrial products, e.g. enzymes, vaccinating antigens, cytokines or
CC	immunoglobulins. Use of (A) eliminates the need for a transposon for gene
CC	insertion; inserted genes do not require promoters and terminators; and
CC	the structure of flanking sequences in (A) ensures universal
CC	applicability. Also any selection marker in (A) can be eliminated by
CC	homologous recombination. (A) provides efficient and stable expression of
CC	genes without causing any functional alterations. This sequence

CC represents an example of the vector of the invention.
XX
SQ Sequence 5834 BP; 1586 A; 1288 C; 1402 G; 1558 T; 0 U; 0 Other;
Query Match 91.7%; Score 122; DB 12; Length 5834;
Best Local Similarity 99.3%; Pred. No. 8.5e-33;
Matches 133; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
1 GCTCCCCCGCGCTTCATAGATGATGATAGAGGCTCGTGGATTGACGTGAGGGG 60
DB 1918 GCTCCCCCGCGCTTCATAGATGATGATAGAGGCTCGTGGATTGACGTGAGGGG 1977
QY 61 CAGGATGCTATTA-TTCTGGAGCGAACTCCGGGCGAATACGAACGCTTGATACAGT 119
DB 1978 CAGGATGCTATTA-TTCTGGAGCGAACTCCGGGCGAATACGAACGCTTGATACAGT 2037
QY 120 TGTAGGAGGAGATT 133
DB 2038 TGTAGGAGGAGATT 2051

RESULT 14
ADM01293
ID ADM01293 standard; DNA; 6465 BP.
XX
AC ADM01293;
XX
DT 01-JUL-2004 (first entry)
XX
DE Plasmid pVTPA-Bar DNA sequence.
XX
XX vector; plasmid; artificial intergene region; plant;
KM transplastomic angiosperm; agronomic property; stress resistance;
KW rbcL gene; ds.
XX
OS Unidentified.
XX
PN WO2004029256-A2.
XX
PD 08-APR-2004.
XX
PF 15-SEP-2003; 2003WO-CU000009.
XX
PR 27-SEP-2002; 2002CU-00000208.
XX
PA (INGG-) CENT ING GENETICA & BIOTECNOLOGIA.
XX
PI Selman-Housein Sosa G, Aguiar Cabeza E, Gonzalez Quintero ADC;
PI Ramos Gonzalez O;
XX
DR WPI; 2004-316131/29.
XX
PT DNA vector for transformation and expression in plastids, useful e.g. for
PT producing pharmaceutical proteins or improving agronomic properties, has
PT gene inserted in artificial intergene region.
XX
PS Example 9; SEQ ID NO 25; 74pp; Spanish.
XX
XX The invention relates to a DNA vector (A) for stable transformation and
CC expression of genes (1) in plastids, where (1) is inserted in an
CC artificial intergene region (AIR) formed by combining two 5'-untranslated
CC regions (5'-UTRs) of genes that transcribe in different directions and
CC are derived from plants of different divisions or classes. (A) are used
CC to produce transplastomic angiosperms that have improved agronomic
CC properties (e.g. resistance to biotic or abiotic stress) or express a
CC very wide range of agricultural, veterinary, pharmaceutical, nutritional
CC or industrial products, e.g. enzymes, vaccinating antigens, cytokines or
CC immunoglobulins. Use of (A) eliminates the need for a transposon for gene
CC insertion; inserted genes do not require promoters and terminators; and
CC the structure of flanking sequences in (A) ensures universal
CC applicability. Also any selection marker in (A) can be eliminated by
CC homologous recombination. (A) provides efficient and stable expression of
CC genes without causing any functional alterations. This sequence

CC represents the plasmid pVTPA-Bar, an example of the vector of the
CC invention.
XX
SQ Sequence 6465 BP; 1705 A; 1503 C; 1602 G; 1655 T; 0 U; 0 Other;
Query Match 91.7%; Score 122; DB 12; Length 6465;
Best Local Similarity 99.3%; Pred. No. 8.8e-33;
Matches 133; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
1 GCTCCCCCGCGCTTCATAGATGATGATAGAGGCTCGTGGATTGACGTGAGGGG 60
DB 1918 GCTCCCCCGCGCTTCATAGATGATGATAGAGGCTCGTGGATTGACGTGAGGGG 1977
QY 61 CAGGATGCTATTA-TTCTGGAGCGAACTCCGGGCGAATACGAACGCTTGATACAGT 119
DB 1978 CAGGATGCTATTA-TTCTGGAGCGAACTCCGGGCGAATACGAACGCTTGATACAGT 2037
QY 120 TGTAGGAGGAGATT 133
DB 2038 TGTAGGAGGAGATT 2051

RESULT 15
ADM01290
ID ADM01290 standard; DNA; 6659 BP.
XX
AC ADM01290;
XX
DT 01-JUL-2004 (first entry)
XX
DE Plasmid pVTPA-aada DNA sequence.
XX
XX vector; plasmid; artificial intergene region; plant;
KM transplastomic angiosperm; agronomic property; stress resistance;
KW rbcL gene; ds.
XX
OS Unidentified.
XX
PN WO2004029256-A2.
XX
PD 08-APR-2004.
XX
PF 15-SEP-2003; 2003WO-CU000009.
XX
PR 27-SEP-2002; 2002CU-00000208.
XX
PA (INGG-) CENT ING GENETICA & BIOTECNOLOGIA.
XX
PI Selman-Housein Sosa G, Aguiar Cabeza E, Gonzalez Quintero ADC;
PI Ramos Gonzalez O;
XX
DR WPI; 2004-316131/29.
XX
PT DNA vector for transformation and expression in plastids, useful e.g. for
PT producing pharmaceutical proteins or improving agronomic properties, has
PT gene inserted in artificial intergene region.
XX
PS Example 3; SEQ ID NO 22; 74pp; Spanish.
XX
XX The invention relates to a DNA vector (A) for stable transformation and
CC expression of genes (1) in plastids, where (1) is inserted in an
CC artificial intergene region (AIR) formed by combining two 5'-untranslated
CC regions (5'-UTRs) of genes that transcribe in different directions and
CC are derived from plants of different divisions or classes. (A) are used
CC to produce transplastomic angiosperms that have improved agronomic
CC properties (e.g. resistance to biotic or abiotic stress) or express a
CC very wide range of agricultural, veterinary, pharmaceutical, nutritional
CC or industrial products, e.g. enzymes, vaccinating antigens, cytokines or
CC immunoglobulins. Use of (A) eliminates the need for a transposon for gene
CC insertion; inserted genes do not require promoters and terminators; and
CC the structure of flanking sequences in (A) ensures universal
CC applicability. Also any selection marker in (A) can be eliminated by
CC homologous recombination. (A) provides efficient and stable expression of
CC

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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: April 17, 2006, 23:37:51 ; Search time 2233 Seconds
(without alignments)
3385.660 Million cell updates/sec

Title: US-10-663-241-32

Perfect score: 133
Sequence: 1 gctcccccgcgcgtcgtcaaa.....tacagtcgtaggagggatt 133

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenBank! :
1: gb_ba : *
2: gb_in : *
3: gb_env : *
4: gb_om : *
5: gb_ov : *
6: gb_pat : *
7: gb_ph : *
8: gb_pr : *
9: gb_ro : *
10: gb_sts : *
11: gb_sy : *
12: gb_un : *
13: gb_vl : *
14: gb_hcg : *
15: gb_pl : *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	133	100.0	133	6	BD106711
2	133	100.0	133	6	AR403658
3	122	91.7	176	6	CO797808
4	122	91.7	1143	6	AR368829
5	122	91.7	1148	6	CO830289
6	122	91.7	1330	6	CO828070
7	122	91.7	1332	6	CO830287
8	122	91.7	1417	6	AR368830
9	122	91.7	3136	11	AF061065
10	122	91.7	4126	11	XXU12814
11	122	91.7	4126	11	XXU12815
12	122	91.7	4304	11	AY005806
13	122	91.7	5834	6	CO797809
14	122	91.7	6465	6	CO797819
15	122	91.7	6659	6	CO797816
16	122	91.7	7454	11	CTR312391
17	122	91.7	7549	6	CO797818
18	122	91.7	7626	11	CTR312392

C	19	122	91.7	7626	11	CTR312393	AJ312393 Chloropia
C	20	122	91.7	8483	11	AY895148	AY895148 Chloropia
C	21	122	91.7	9731	11	AY442171	AY442171 Chloropia
C	22	121	91.0	300	6	AR171710	AR171710 Sequence
C	23	121	91.0	300	6	AR171711	AR171711 Sequence
C	24	121	91.0	1183	6	BD235370	BD235370 Translati
C	25	121	91.0	1327	6	CO828069	CO828069 Sequence
C	26	121	91.0	1613	6	CO830293	CO830293 Sequence
C	27	121	91.0	4508	11	AY575999	AY575999 Chloropia
C	28	121	91.0	4671	6	BD235379	BD235379 Translati
C	29	117.8	88.6	4591	6	BD174931	BD174931 A system
C	30	114.8	86.3	142	6	BD174932	BD174932 A system
C	31	110	82.7	7039	11	DQ073476	DQ073476 Chloropia
C	32	107	80.5	119	15	CS001461	CS001461 Sequence
C	33	102.8	77.3	184	6	AR145914	AR145914 Sequence
C	34	102.8	77.3	201	6	AR242682	AR242682 Sequence
C	35	102.8	77.3	220	6	BD180933	BD180933 Method of
C	36	102.8	77.3	220	6	AX537601	AX537601 Sequence
C	37	102.8	77.3	2113	15	CHNT8M1	V00165 Tobacco chl
C	38	102.8	77.3	2962	11	XXU12809	U12810 Transformat
C	39	102.8	77.3	3019	11	XXU12810	U12810 Transformat
C	40	102.8	77.3	3019	11	XXU12811	U12811 Transformat
C	41	102.8	77.3	3274	15	CHNPT8M1	X70938 N.Plumbagin
C	42	102.8	77.3	4174	11	XXU12812	U12812 Transformat
C	43	102.8	77.3	4363	6	AX798125	U14813 Transformat
C	44	102.8	77.3	4363	6	AX798125	AX798125 Sequence
C	45	102.8	77.3	4363	6	AX798909	AX798909 Sequence

ALIGNMENTS

RESULT 1	BD106711	133 bp	DNA	linear	PAT 18-SEP-2002
LOCUS	BD106711				
DEFINITION	Plastid promoters for transgene expression in the plastids of higher plants.				
ACCESSION	BD106711				
VERSION	BD106711.1 GI:23201529				
KEYWORDS	JP 2002502262-A/32.				
SOURCE	synthetic construct				
ORGANISM	other sequences; artificial sequences.				
REFERENCE	1 (bases 1 to 133)				
AUTHORS	Maliga, P., Silhavy, D. and Stryman, P.				
TITLE	Plastid promoters for transgene expression in the plastids of higher plants				
JOURNAL	Patent: JP 2002502262-A 32 22-JAN-2002;				
COMMENT	RUTGERS THE STATE UNIVERSITY OF NEW JERSEY PN JP 2002502262-A/32				
	PD 22-JAN-2002				
	PF 03-JUN-1998 JP 1999502824				
	PR 03-JUN-1997 US 60/048376, 12-SEP-1997 US 60/058670 PI				
	PAL MALIGA, DANIEL, SILHAVY, PRIYA STRIMAN				
	PC C12N5/04, C12N15/00, C12N15/09, C12N15/29, C12N15/82, A01H1/00, PC				
	A01H3/00,				
	PC A01H5/00				
	CC Strandedness: Single;				
	CC Key Location/Qualifiers.				
FEATURES	source				
	1..133				
	/organism="synthetic construct"				
	/mol_type="genomic DNA"				
	/db_xref="taxon:32630"				
ORIGIN					
Query Match	100.0%; Score 133; DB 6; Length 133;				
Best Local Similarity	100.0%; Pred. No. 1e-33;				
Matches	133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
QY	1 GCTCCCCCGCGCTGTTCAATGAGATGATGAGGCTGTGGATTGACTGAGGGG 60				
DB	1 GCTCCCCCGCGCTGTTCAATGAGATGATGAGGCTGTGGATTGACTGAGGGG 60				

ORIGIN

Query Match 100.0%; Score 133; DB 6; Length 133;
Best Local Similarity 100.0%; Pred. No. 1e-33;
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCCCCCGCGTCTCAATGAGATGAGATGAGGCTCGTGGATTGACGTGAGGGG 60
Db 1 GCTCCCCCGCGTCTCAATGAGATGAGATGAGGCTCGTGGATTGACGTGAGGGG 60

Qy 61 CAGGATGAGCTATATTCTGGAGCGAAGCTCCGGGCGAATACGAAACGCTTGATACAGTT 120
Db 61 CAGGATGAGCTATATTCTGGAGCGAAGCTCCGGGCGAATACGAAACGCTTGATACAGTT 120

Qy 121 GTAGGAGAGGATT 133
Db 121 GTAGGAGAGGATT 133

RESULT 2
LOCUS AR403658 133 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 32 from patent US 6624296.
ACCESSION AR403658
VERSION AR403658.1 GI:40151276
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 133)
AUTHORS Maliga,P., Silhavy,D. and Sriaman,P.
TITLE Plasmid promoters for transgene expression in the plasmids of higher plants
JOURNAL Patent: US 6624296-A 32 23-SEP-2003;
Rutgers, The State University of New Jersey; East Brunswick, NJ
FEATURES
SOURCE 1..133
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 100.0%; Score 133; DB 6; Length 133;
Best Local Similarity 100.0%; Pred. No. 1e-33;
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCCCCCGCGTCTCAATGAGATGAGATGAGGCTCGTGGATTGACGTGAGGGG 60
Db 1 GCTCCCCCGCGTCTCAATGAGATGAGATGAGGCTCGTGGATTGACGTGAGGGG 60

Qy 61 CAGGATGAGCTATATTCTGGAGCGAAGCTCCGGGCGAATACGAAACGCTTGATACAGTT 120
Db 61 CAGGATGAGCTATATTCTGGAGCGAAGCTCCGGGCGAATACGAAACGCTTGATACAGTT 120

Qy 121 GTAGGAGAGGATT 133
Db 121 GTAGGAGAGGATT 133

RESULT 3
LOCUS CQ797808 176 bp DNA linear PAT 20-APR-2004
DEFINITION Sequence 14 from Patent WO2004029256.
ACCESSION CQ797808
VERSION CQ797808.1 GI:46426081
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 other sequences; artificial sequences.
AUTHORS belman-houstein Sosa,G., aguiar Cabeza,E., gonz lez Quintero,A.D. and ramos gonz lez,O.
TITLE Vector for the production of transplastomic angiosperm plants
JOURNAL Patent: WO 2004029256-A 14 08-APR-2004;
CENTRO DE INGENIERIA GENETICA Y BIOTECNOLOGIA (CU)
FEATURES
SOURCE 1..176
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Description of Artificial Sequence: Synthetic DNA fragment codifying for the promoter region of the plasmid 16S ribosomal RNA (Prm), with added restriction sites."

ORIGIN

Query Match 91.7%; Score 122; DB 6; Length 176;
Best Local Similarity 99.3%; Pred. No. 5.3e-30;
Matches 133; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 GCTCCCCCGCGTCTCAATGAGATGAGATGAGGCTCGTGGATTGACGTGAGGGG 60
Db 16 GCTCCCCCGCGTCTCAATGAGATGAGATGAGGCTCGTGGATTGACGTGAGGGG 75

Qy 61 CAGGATGAGCTATATTCTGGAGCGAAGCTCCGGGCGAATACGAAACGCTTGATACAGT 119
Db 76 CAGGATGAGCTATATTCTGGAGCGAAGCTCCGGGCGAATACGAAACGCTTGATACAGT 135

Qy 120 TGTAGGAGAGGATT 133
Db 136 TGTAGGAGAGGATT 149

RESULT 4
LOCUS AR368829/c 1143 bp DNA linear PAT 12-SEP-2003
DEFINITION Sequence 6 from patent US 6376744.
ACCESSION AR368829
VERSION AR368829.1 GI:34603191
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1143)
AUTHORS Maliga,P., Sikdar,S. and Reddy,S.V.
TITLE Plasmid transformation in Arabidopsis thaliana
JOURNAL Patent: US 6376744-A 6 23-APR-2002;
Rutgers, The State University of New Jersey; New Brunswick, NJ
FEATURES
SOURCE 1..1143
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 91.7%; Score 122; DB 6; Length 1143;
Best Local Similarity 99.3%; Pred. No. 5.9e-30;
Matches 133; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 GCTCCCCCGCGTCTCAATGAGATGAGATGAGGCTCGTGGATTGACGTGAGGGG 60
Db 1130 GCTCCCCCGCGTCTCAATGAGATGAGATGAGGCTCGTGGATTGACGTGAGGGG 1071

Qy 61 CAGGATGAGCTATATTCTGGAGCGAAGCTCCGGGCGAATACGAAACGCTTGATACAGT 119
Db 1070 CAGGATGAGCTATATTCTGGAGCGAAGCTCCGGGCGAATACGAAACGCTTGATACAGT 1011

Qy 120 TGTAGGAGAGGATT 133
Db 1010 TGTAGGAGAGGATT 997

RESULT 5
LOCUS CQ830289 1148 bp DNA linear PAT 12-JUL-2004
DEFINITION Sequence 3 from Patent WO2004055191.
ACCESSION CQ830289
VERSION CQ830289.1 GI:50250782
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 other sequences; artificial sequences.
AUTHORS Tiasot,G., Wisniewski,J.P. and Ferrillo,J.M.
TITLE Expression of hydroxyphenylpyruvate dioxygenase in plasmids of plants for herbicide tolerance
JOURNAL Patent: WO 2004055191-A 3 01-JUL-2004;
Biogenma (FR)

FEATURES

source

Location/Qualifiers

1. .1148

/organism="synthetic construct"

/mol_type="unassigned DNA"

/db_xref="taxon:32630"

/note="Synthetic construct"

1. .117

/note="Prm"

118. .135

/note="5'rbcl"

136. .930

/note="unnamed protein product; aadA"

/codon_start=1

/transl_table=11

/protein_id="CAH04014.1"

/db_xref="GI:50250783"

/translation="MDPEAVIAVSTQLSRVGVIRHLEPTLLAVHLYGSADVGLK
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PAKRELQFGEWQNDILAGI FEPATIDIDIALILTKARHSVALVGPAAEELPDPYE
ODLFEALNETLTLNMSPPDMAGDERNVVTLISRIYSATVGKIAPDVADAMERLP
AQYOPVILEARQAVLQGEEDRLASRADQLEEFVHYKGIITKVGK"

931. .1148

/note="3'rbcl"

terminator

ORIGIN

Query Match

Best Local Similarity 91.7%; Score 122; DB 6; Length 1148;

Matches 133; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 GCTCCCGCCGCTGTTCAATGAGATGAAGAGAGGCTCGTGAGATTGACGTGAGGGG 60

Db 1 GCTCCCGCCGCTGTTCAATGAGATGAAGAGAGGCTCGTGAGATTGACGTGAGGGG 60

Qy 61 CAGGATGGCTATA-TTCTGGAGCGCACTCCGGGCGAATACGCGCTTGATCACT 119

Db 61 CAGGATGGCTATAATTCTGGAGCGCACTCCGGGCGAATACGCGCTTGATCACT 120

Qy 120 TGTAGGAGGAGATT 133

Db 121 TGTAGGAGGAGATT 134

RESULT 6

LOCUS CQ828070 1330 bp DNA linear PAT 05-JUL-2004

DEFINITION Sequence 11 from Patent WO2004053133.

ACCESSION CQ828070

VERSION CQ828070.1 GI:49731589

KEYWORDS

SOURCE

ORGANISM

synthetic construct

synthetic construct

other sequences; artificial sequences.

REFERENCE

AUTHORS

1 Tisot,G., Dufourmantel,N., Garcon,F., Ferrillo,J.M. and Pellissier,B.

TITLE

Fertile transplastomic leguminous plants

JOURNAL

Patent: WO 2004053133-A 11 24-JUN-2004;

FEATURES

source

1. .1330

/organism="synthetic construct"

/mol_type="unassigned DNA"

/db_xref="taxon:32630"

/note="AADA166"

ORIGIN

Query Match

Best Local Similarity 91.7%; Score 122; DB 6; Length 1330;

Matches 133; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 GCTCCCGCCGCTGTTCAATGAGATGAAGAGGCTCGTGAGATTGACGTGAGGGG 60

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Qy 61 CAGGATGGCTATA-TTCTGGAGCGCACTCCGGGCGAATACGAGCGCTTGATCACT 119

Db 61 CAGGATGGCTATAATTCTGGAGCGCACTCCGGGCGAATACGAGCGCTTGATCACT 120

Qy 120 TGTAGGAGGAGATT 133

Db 121 TGTAGGAGGAGATT 134

RESULT 7

LOCUS CQ830287 1332 bp DNA linear PAT 12-JUL-2004

DEFINITION Sequence 1 from Patent WO2004055191.

ACCESSION CQ830287

VERSION CQ830287.1 GI:50250780

KEYWORDS

SOURCE

ORGANISM

synthetic construct

synthetic construct

other sequences; artificial sequences.

REFERENCE

AUTHORS

1 Tisot,G., Wisniewski,J.P. and Ferrillo,J.M.

TITLE

Expression of hydroxyphenylpyruvate dioxygenase in plaetids of plants for herbicide tolerance

JOURNAL

Patent: WO 2004055191-A 1 01-JUL-2004;

Biogemma (PR)

FEATURES

source

Location/Qualifiers

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/organism="synthetic construct"

/mol_type="unassigned DNA"

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/note="Synthetic construct"

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/note="Prm"

118. .135

/note="5'rbcl"

136. .930

/note="unnamed protein product; aadA"

/codon_start=1

/transl_table=11

/protein_id="CAH04013.1"

/db_xref="GI:50250781"

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ODLFEALNETLTLNMSPPDMAGDERNVVTLISRIYSATVGKIAPDVADAMERLP
AQYOPVILEARQAVLQGEEDRLASRADQLEEFVHYKGIITKVGK"

937. .1332

/note="3'psbA"

terminator

ORIGIN

Query Match

Best Local Similarity 91.7%; Score 122; DB 6; Length 1332;

Matches 133; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 GCTCCCGCCGCTGTTCAATGAGATGAAGAGGCTCGTGAGATTGACGTGAGGGG 60

Db 1 GCTCCCGCCGCTGTTCAATGAGATGAAGAGGCTCGTGAGATTGACGTGAGGGG 60

Qy 61 CAGGATGGCTATA-TTCTGGAGCGCACTCCGGGCGAATACGAGCGCTTGATCACT 119

Db 61 CAGGATGGCTATAATTCTGGAGCGCACTCCGGGCGAATACGAGCGCTTGATCACT 120

Qy 120 TGTAGGAGGAGATT 133

Db 121 TGTAGGAGGAGATT 134

RESULT 8

LOCUS AR368830 1417 bp DNA linear PAT 12-SEP-2003

DEFINITION Sequence 7 from patent US 6376744.

ACCESSION AR368830

VERSION AR368830.1 GI:34603192
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1417)
AUTHORS Maliga, P., Sikdar, S. and Reddy, S. V.
TITLE Plasmid transformation in Arabidopsis thaliana
JOURNAL Patent: US 6376744-A 7 23-APR-2002;
Rutgers, The State University of New Jersey; New Brunswick, NJ
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source
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/mol_type="genomic DNA"
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Best Local Similarity 99.3%; Pred. No. 66-30; Mismatches 0; Indels 1; Gaps 1;
Matches 133; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1 GCTCCCCCGCGCTCGTTCATAGATGATGAAGAGCTCGTGGATTGACGTGAGGGG 60
DB 23 GCTCCCCCGCGCTCGTTCATAGATGATGAAGAGCTCGTGGATTGACGTGAGGGG 82
QY 61 CAGGATGGCTATA-TTCTGGAGCGAAGCTCCGGCGAATGCAAGCGCTTGATACAGT 119
DB 83 CAGGATGGCTATA-TTCTGGAGCGAAGCTCCGGCGAATGCAAGCGCTTGATACAGT 142
QY 120 TGTAGGAGGAGATT 133
DB 143 TGTAGGAGGAGATT 156
RESULT 9
AF061065/c
LOCUS AF061065 3136 bp DNA linear SYN 14-NOV-1998
DEFINITION Plasmid transformation vector pGS31A 16S ribosomal RNA gene,
partial sequence; aminoglycoside 3'-adenyltransferase (aadA) gene,
complete cds.
ACCESSION AF061065
VERSION AF061065.1 GI:3859840
KEYWORDS Plasmid transformation vector pGS31A
SOURCE Plasmid transformation vector pGS31A
ORGANISM Plasmid transformation in Arabidopsis thaliana
REFERENCE 1 (bases 1 to 3136)
AUTHORS Svab, Z. and Maliga, P.
TITLE High-frequency plasmid transformation in tobacco by selection for a
chimeric aadA gene
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 90 (3), 913-917 (1993)
PUBMED 8381537
REFERENCE 2 (bases 1 to 3136)
AUTHORS Sikdar, S.R., Serino, G., Chaudhuri, S. and Maliga, P.
TITLE Plasmid transformation in Arabidopsis thaliana
JOURNAL Plant Cell Rep. 18, 20-24 (1998)
REFERENCE 3 (bases 1 to 3136)
AUTHORS Serino, G. and Maliga, P.
TITLE Direct Submision
JOURNAL Submitted (22-APR-1998) Waksman Institute, Rutgers University, 190
Frelinghuysen Road, Piscataway, NJ 08854-8020, USA
FEATURES
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/mol_type="genomic DNA"
/db_xref="taxon:83809"
/note="Plasmid transformation vector, targeting insertions
into the inverted repeat region of the plasmid genome"
misc_feature 1..1058
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rRNA complement (<1..599)
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tRNA complement (831..902)
/product="tRNA-Val"

misc_feature complement (1059..2201)
/note="chimeric aadA gene in a tobacco plasmid expression
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3'UTR /citation= [1]
gene complement (1059..1247)
/note="plasmid pabA"
CDS complement (1262..2053)
/gene="aadA"
complement (1262..2053)
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spectinomycin by adenylating the antibiotics"
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/db_xref="GI:3859841"
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AKRELQGEWQRNDILAGIPEPATIDIDLAILTKARSHSVAVGPAAEELFDVLEQ
DLFEALNETLTLNMSPPDMAGDERNVVLTLSRIWYSAVTGKIAEDVADAMERLPA
QYQVILAEARQAYIGOEEDRLASPADQLSEFVHYVKGSEITKVQK"
complement (2054..2188)
/note="Chimeric promoter based on the promoter of the rRNA
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misc_feature /citation= [1]
2193..2198
/note="KpnI cloning site"
misc_feature 2202..3136
/note="Arabidopsis thaliana plasmid DNA"
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Query Match 91.7%; Score 122; DB 11; Length 3136;
Best Local Similarity 99.3%; Pred. No. 63e-30; Mismatches 0; Indels 1; Gaps 1;
Matches 133; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1 GCTCCCCCGCGCTCGTTCATAGATGATGAAGAGCTCGTGGATTGACGTGAGGGG 60
DB 2188 GCTCCCCCGCGCTCGTTCATAGATGATGAAGAGCTCGTGGATTGACGTGAGGGG 2129
QY 61 CAGGATGGCTATA-TTCTGGAGCGAAGCTCCGGCGAATGCAAGCGCTTGATACAGT 119
DB 2128 CAGGATGGCTATA-TTCTGGAGCGAAGCTCCGGCGAATGCAAGCGCTTGATACAGT 2069
QY 120 TGTAGGAGGAGATT 133
DB 2068 TGTAGGAGGAGATT 2055
RESULT 10
XXU12814/c
LOCUS XXU12814 4126 bp DNA linear SYN 24-MAY-1995
DEFINITION Transformation vector pPRV112A, plasmid targeting segment.
ACCESSION U12814
VERSION U12814.1 GI:559552
KEYWORDS Cloning vector pPRV112A
SOURCE Cloning vector pPRV112A
ORGANISM Cloning vector pPRV112A
REFERENCE 1 (bases 1 to 4126)
AUTHORS Zoubenko, O.V., Allison, L.A., Svab, Z. and Maliga, P.
TITLE Efficient targeting of foreign genes into the tobacco plasmid
genome
JOURNAL Nucleic Acids Res. 22 (19), 3819-3824 (1994)
PUBMED 7937099
REFERENCE 2 (bases 1 to 4126)
AUTHORS Hajdukiewicz, P. T.
TITLE Direct Submision
JOURNAL Submitted (01-AUG-1994) Peter T. Hajdukiewicz, Waksman Inst.,
Rutgers University, Old Hoes Lane, Piscataway, NJ 08855, USA
FEATURES
source
1..4126
/organism="Cloning vector pPRV112A"
/mol_type="genomic DNA"

[illegible]

Query Match	91.7%	Score 122;	DB 11;	Length 4126;
Best Local Similarity	99.3%;	Pred. No. 6.4e-30;		
Matches 133; Conservative	0;	Mismatches 0;	Indels 1;	Gaps 1

QY	1	GCTCCCCCGCGTCCGTTCAATGAGAAATGAGATGAAGAGCTCGGAGATTTGACCTGAGAGGGG	60
Db	2888	GCTCCCCCGCGTCCGTTCAATGAGAAATGAGATGAAGAGCTCGGAGATTTGACCTGAGAGGGG	282
QY	61	CAGGGATGGCTATA-TTCGTGGGAGGGAACCTCCGGCGAAATGAGAGCCCTGGATATACAT	119
Db	2828	CAGGGATGGCTATATTTCTGGAGCGAATCTCCGGCGAAATGAGAGCCCTGGATATACAT	276
QY	120	TGTATGGAGGGGATT	133
Db	2768	TGTATGGAGGGGATT	2755

RESULT 11				
LOCUS	XXU12815/c			
DEFINITION	Transformation vector pPRV112b, plastid targeting segment.	4126 bp	DNA	linear
ACCESSION	U12815			SYN 24-MAY-1994
VERSION	U12815.1			
KEYWORDS	GI:559554			
SOURCE				
ORGANISM				
REFERENCE				
AUTHORS				
TITLE				
JOURNAL				
PUBMED				
REFERENCE				
AUTHORS				
TITLE				
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JOURNAL				

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misc_feature	/translation="MAEFAVIAEVSTQSEVGVIERHLEPTLAVHLYGSAVDGGLKAKRERLOGEWGRNDILAGIRPEPATIDIDLAILTKARBHSVALGPAAEELPFDVLREGDYLPAALIEITLWNSPPDMAGDERNVALLTSRIYSAYVTGKIAPDVADAAMBERLLPQQYQFVILEARQAATGYQEEDRIASRADQLEEFVHVHKGEBITKVGG"
misc_feature	2894..2950 /note="multiple cloning site: HindIII, PstI, SalI, XbaI, SmaI, KpnI, SacI, EcoRI"
misc_feature	2951..4126 /note="similar to part of tobacco chloroplast repeat region, GenBank Accession Number Z00044"
ORIGIN	

	Query Match	Best Local Similarity	91.7%; 99.3%;	Score 122; Pred. No. 6.4e-30/	DB 11; Mismatches 0;	Length 4126; Indels 1;	Gaps 1,
Qy	1	GCTCCCCCGCGTGGTTCAATGAGAAATGAAGAGGCTCGTGGAATTGACGTGAGGGGG					60
Db	2888	GCTCCCCCGCGTGGTTCGTAATGAGAATGGAATAAGAGCTCGTGGAATTGACTGACGGGG					28229
Qy	61	CAGGAGATGGCTAAT-TTCTGGAGCCGAACCTCCGGCCGAATACGAAGCGCTTGGATPACAGT					119
Db	2828	CAGGAGATGGCTAATTTCTGGAGCCGAACCTCCGGCCGAATACGAAGCGCTTGGATPACAGT					27659
Qy	120	TGTAGGAGGGGATT	133				
Db	2768	TGTAGGAGGGGATT	2755				

RESULT	12
AY005806/c	
LOCUS	AY005806 4304 bp DNA linear SYN 28-JAN-2002
DEFINITION	Transformation vector pUTS54, plasmid targeting region.
ACCESSION	AY005806
VERSION	AY005806.1 GI:10442803
KEYWORDS	.
SOURCE	synthetic construct
ORGANISM	synthetic construct
REFERENCE	other sequences; artificial sequences.
AUTHORS	1 (bases 1 to 4304)
TITLE	Suzuki,U.Y. and Malinga,P.
JOURNAL	Engineering of the rpl23 gene cluster to replace the plasmid RNA
PUBMED	polymerase alpha subunit with the Escherichia coli homologue
REFERENCE	Curr. Genet. 38 (4), 218-225 (2000)
	11126781
	2 (bases 1 to 4304)

AUTHORS Suzuki, J.Y. and Maliga, P.
TITLE Direct Submission
JOURNAL Submitted (26-JUL-2000) Waksman Institute, Rutgers University, 190
Frelinghuysen Road, Piscataway, NJ 08854, USA
FEATURES
SOURCE Location/Qualifiers
1. .4304
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/focus
/note="targeting region of plasmid transformation vector
pJY554 in the Nicotiana tabacum plasmid"
1. .1417
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/organelle="plastid"
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/db_xref="taxon:4097"
1427. .1648
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/organelle="plastid"
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1657. .2448
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/organism="Nicotiana tabacum"
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/db_xref="GI:10442804"
/translation="MGVTKKPNDLPVLRATKAGMGNYYGEPAMPNDLYIPVVI
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complement(1663. .2469)
/gene="aadA"
/note="confers streptomycin and spectinomycin resistance
to plants"
/codon_start=1
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/protein_id="AAG15581.1"
/db_xref="GI:10442808"
/translation="MSPTGSAVIAVSTOLSEVGVIERHLEPTLLAVHLYGSAV
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PMRYAKRELPGEWQRNDIAGIFEPATIDIALITLKAREHSVALVGRASELPD
FVPEODLFEALNETLITMNSPPDMAGDERNVLTLSRIWYSAVTKIAPKOVADWAM

promoter
2487. .2604
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misc_feature
2637. .4304
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/product="RNA polymerase alpha subunit"
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/db_xref="GI:10442805"
/translation="MVREKLVSTRTLLQMKCVESRTDSKRLYYGRFILSPMKGOADT
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TPHNFQDSYPTIDAVFMPVRNANSHSYGNKQKELPLEITNSLITPKALHEA
SRNIDLPFIPLEHEDNLYIQDQHTVPLSPFPHDLAKLTKKKKIALKSLFTIQ
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NK"

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/db_xref="GI:10442806"
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/db_xref="GI:10442807"
/translation="LIRRRGRITVTCNPPHKKQG"

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ORIGIN

Query Match 91.7%; Score 122; DB 11; Length 4304;
Best Local Similarity 99.3%; Pred. No. 6.4e-30;
Matches 133; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 GCTCCCCCGCGGTCGATGAGATGATGAGAGGCTCGTGGATTGACGTGAGGGG 60
DB 2604 GCTCCCCCGCGGTCGATGAGATGAGATGAGAGGCTCGTGGATTGACGTGAGGGG 2545
QY 61 CAGGATGCGTATTA-TTCTGGAGACCGAATCCGGCCGAATTCGAAGCGCTTGATACGT 119
DB 2544 CAGGATGCGTATTA-TTCTGGAGACCGAATCCGGCCGAATTCGAAGCGCTTGATACGT 2485
QY 120 TGTAGGAGGAGATT 133
DB 2484 TGTAGGAGGAGATT 2471

RESULT 13
LOCUS CQ797809 5834 bp DNA linear PAT 20-APR-2004
DEFINITION Sequence 15 from Patent WO2004029256.
ACCESSION CQ797809
VERSION CQ797809.1 GI:46426082
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 other sequences; artificial sequences.

AUTHORS selman-housein Sosa,G., aguiar Cabeza,E., gonz lez Quintero,A.D.
and ramos gonz lez,O.
TITLE Vector for the production of transplastomic angiosperm plants
JOURNAL Patent: WO 2004029256-A 15 08-APR-2004;
CENTRO DE INGENIERIA GENETICA Y BIOTECNOLOGIA (CU)

FEATURES
source
1. .5834
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Description of Artificial Sequence: Nucleotide
sequence of DNA fragment from the vector pVTPA between the
rice atpb and tobacco rbcl borders."

ORIGIN

Query Match 91.7%; Score 122; DB 6; Length 5834;
Best Local Similarity 99.3%; Pred. No. 6.5e-30;
Matches 133; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 GCTCCCCCGCGCTTCATAGATGATAGATAGAGGCTCGTGGATTGACGTGAGGGG 60
DB 1918 GCTCCCCCGCGCTTCATAGATGATAGATAGAGGCTCGTGGATTGACGTGAGGGG 1977
QY 61 CAGGATGGCTATA-TTCTGGAGCGCAACTCCGGCGAATACGAGCGCTTGATACAGT 119
DB 1978 CAGGATGGCTATA-TTCTGGAGCGCAACTCCGGCGAATACGAGCGCTTGATACAGT 2037
QY 120 TGTAGGAGGAGATT 133
DB 2038 TGTAGGAGGAGATT 2051

RESULT 14
CQ797819 6465 bp DNA linear PAT 20-APR-2004
LOCUS Sequence 25 from Patent WO2004029256.
ACCESSION CQ797819
VERSION CQ797819.1 GI:46426092
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS selman-housein Sosa,G., aguiar Cabeza,E., gonz lez Quintero,A.D.
and ramos gonz lez,O.
TITLE Vector for the production of transplastomic angiosperm plants
JOURNAL Patent: WO 2004029256-A 25 08-APR-2004;
CENTRO DE INGENIERIA GENETICA Y BIOTECNOLOGIA (CU)
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
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the rice atpb and tobacco rbcl borders."

ORIGIN

Query Match 91.7%; Score 122; DB 6; Length 6465;
Best Local Similarity 99.3%; Pred. No. 6.5e-30;
Matches 133; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 GCTCCCCCGCGCTTCATAGATGATAGATAGAGGCTCGTGGATTGACGTGAGGGG 60
DB 1918 GCTCCCCCGCGCTTCATAGATGATAGATAGAGGCTCGTGGATTGACGTGAGGGG 1977
QY 61 CAGGATGGCTATA-TTCTGGAGCGCAACTCCGGCGAATACGAGCGCTTGATACAGT 119
DB 1978 CAGGATGGCTATA-TTCTGGAGCGCAACTCCGGCGAATACGAGCGCTTGATACAGT 2037
QY 120 TGTAGGAGGAGATT 133
DB 2038 TGTAGGAGGAGATT 2051

RESULT 15

CQ797816 6659 bp DNA linear PAT 20-APR-2004
LOCUS Sequence 22 from Patent WO2004029256.
ACCESSION CQ797816
VERSION CQ797816.1 GI:46426089
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS selman-housein Sosa,G., aguiar Cabeza,E., gonz lez Quintero,A.D.
and ramos gonz lez,O.
TITLE Vector for the production of transplastomic angiosperm plants
JOURNAL Patent: WO 2004029256-A 22 08-APR-2004;
CENTRO DE INGENIERIA GENETICA Y BIOTECNOLOGIA (CU)
FEATURES
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1. .6659
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Description of Artificial Sequence: Nucleotide
sequence of DNA fragment from the vector pVTPA-aada
between the rice atpb and tobacco rbcl borders."

ORIGIN

Query Match 91.7%; Score 122; DB 6; Length 6659;
Best Local Similarity 99.3%; Pred. No. 6.5e-30;
Matches 133; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 GCTCCCCCGCGCTTCATAGATGATAGATAGAGGCTCGTGGATTGACCGGAGGGG 60
DB 1918 GCTCCCCCGCGCTTCATAGATGATAGATAGAGGCTCGTGGATTGACCGGAGGGG 1977
QY 61 CAGGATGGCTATA-TTCTGGAGCGCAACTCCGGCGAATACGAGCGCTTGATACAGT 119
DB 1978 CAGGATGGCTATA-TTCTGGAGCGCAACTCCGGCGAATACGAGCGCTTGATACAGT 2037
QY 120 TGTAGGAGGAGATT 133
DB 2038 TGTAGGAGGAGATT 2051

Search completed: April 18, 2006, 00:23:15
Job time : 2235 secs

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